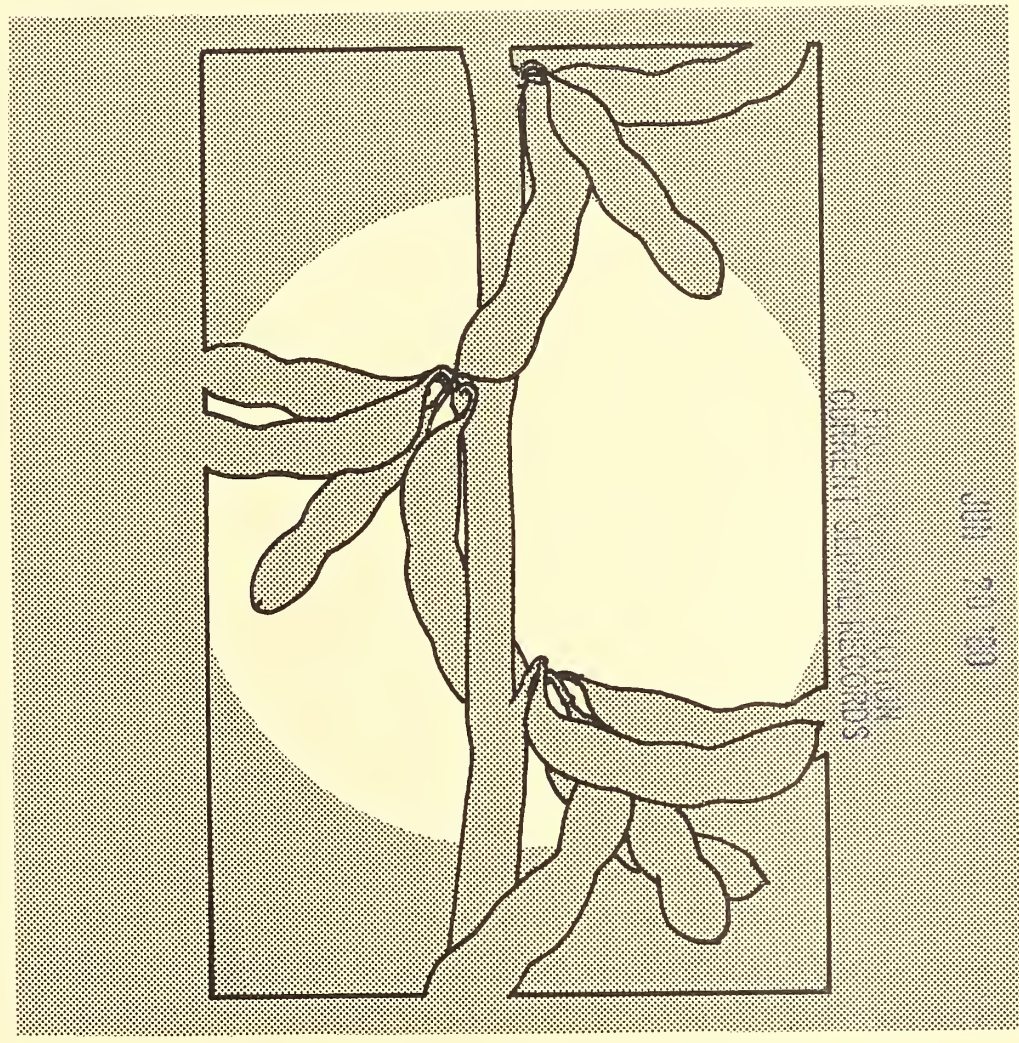


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
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Soybean Genetics Newsletter



Volume 7

April 1980

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Agricultural Research Service - USDA
Department of Agronomy
and Department of Genetics
Iowa State University
Ames, Iowa 50011

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I. FOREWORD

Each October we mail a "flyer" to everyone on the Soybean Genetics Newsletter mailing list, calling for articles, research notes and reports. The articles in Volume 7 give an indication of the universal nature of the response to our request. In our "Rules for Contributors" we state "newsletter articles may be preliminary in nature and speculative in content, and should not be regarded as equivalent to papers in formal scientific journals. Even so, such reports can be exceedingly helpful and valuable if viewed in the proper perspective." The frequency with which Newsletter articles are cited by other authors helps to prove our point.

Every three years, our "Request for Articles" has a "Note to Subscribers" tacked on the bottom. We feel it is necessary to include in our mailing list only those who are really interested in receiving the Newsletter; and to facilitate subscriber response, a coupon is printed, to be signed, torn off and returned to us. The return of these coupons was a bit disappointing. Presumably, many of those who knew they would not be contributing articles or research notes discarded the "flyer" without noticing the coupon for the mailing list. A second mailing, with only the note to subscribers, got almost 100% response.

The Soybean Genetics Newsletter is free UPON REQUEST . . . and even those already on the mailing list MUST RENEW THEIR REQUEST every three years.

Volunteers who made this volume possible were Hollys Heer, Therese Curry, and Teresa Brecht.

R. G. Palmer, Editor

The editors regret inconsistencies in references in several of the research notes. We could not spare time to check all citations at the library.

Mention of a trademark or proprietary product by the USDA or Iowa State University does not imply its approval to the exclusion of other products that may also be suitable.

II. ANNOUNCEMENTS

FOURTH INTERNATIONAL SYMPOSIUM ON NITROGEN FIXATION

The fourth symposium in this series will be held in Canberra, Australia, December 1-5, 1980. All aspects of nitrogen fixation, both chemical and biological, will be considered in a series of interdisciplinary discussions. In addition, there will be extensive poster displays and round-table workshops. There currently is widespread interest in the genetics of the legume-Rhizobium symbiosis, and it is expected that both the host and the bacterial side will receive consideration. For those with ambitions to visit Australia (and remember, December is our summer), now is the time. Further details from:

Dr. A. H. Gibson, Chairman
Organizing Committee
Division of Plant Industry
CSIRO
P.O. Box 1600
Canberra City A.C.T. 2601
AUSTRALIA

New Officers for Commercial Soybean Breeders

New officers for the Commercial Soybean Breeders organization are: Chairman of the Executive Committee--Harry B. Collins, Delta & Pine Land Co., Scott, MS 38772, (601)742-3351; and Secretary of the Executive Committee--Charles Laible, Funks Seed International, 1300 W. Washington St., P.O. Box 2911, Bloomington, IL 61701, (309)829-9461.

SOYBEAN RUST NEWSLETTER

The third volume of the Soybean Rust Newsletter is being published by International Working Group on Soybean Rust and will be available in April 1980. Single copies of the newsletter can be obtained free by writing to:

Mr. S. Shanmugasundaram
Secretary, IWGSR
AVRDC, P.O. Box 42
Shanhua, Tainan 741, Taiwan
REPUBLIC of CHINA

Request for contributions to the fourth issue of "Soybean Rust Newsletter"

Research articles, reports, notes, announcement of resistant or tolerant germplasm, and any other news item related to soybean rust are requested, and they will be accepted until November 1980. Address all correspondence regarding the SRN to the above address.

Rules for contributions

- 1) Information in the SRN will be informal to stimulate the exchange of ideas and information among soybean rust scientists. SRN articles may be preliminary in nature and speculative in content, and should not be regarded as equivalent to papers published in formal scientific journals. Even so, such reports can be very valuable and helpful, if viewed in the proper perspective. Data presented in the SRN are not to be used in other publications without the consent of the respective authors.
- 2) Contributions should be in English, typed double spaced on 8½" by 11" pages. You may send as many separate contributions as you wish. Send two copies for each article.
- 3) Correspondence regarding an article should be on a separate page.
- 4) Photographs should be glossy black/white prints of high quality with good dark and light contrasts. Drawings for graphs and charts should be prepared with India ink on good quality tracing paper. Typewritten matter is not usually acceptable on graphs and charts. A good size for photographs is 5" by 7" and drawings is what will fit on an 8½" by 11" page.
- 5) Except for possible minor editing, manuscripts will be published as received from contributors.

- 6) Title your report, place your name(s), name of university, institution or company under the title. Please give complete address. (For contributors outside Taiwan (R.O.C.), please send reports by airmail.)
- 7) Citations of recent publications on soybean rust are specifically solicited.

III. REPORT OF THE SOYBEAN GENETICS COMMITTEE

A) The current members of this committee and the expiration dates of their terms are as follows:

R. L. Bernard, USDA (1982)
Turner Hall
Department of Agronomy
University of Illinois
Urbana, IL 61801

T. E. Devine, USDA (1982)
CCNFL, Bldg. 001
BARC-West
Beltsville, MD 20705

E. T. Gritton (1983)
Department of Agronomy
University of Wisconsin
Madison, WI 53706

T. Hymowitz (1981)
Department of Agronomy
University of Illinois
Urbana, IL 61801

C. Newell (1983)
Department of Agronomy
University of Illinois
Urbana, IL 61801

R. G. Palmer, USDA (Ex-Officio)
(Editor of Soybean Genetics
Newsletter)
Department of Genetics
Iowa State University
Ames, IA 50011

J. R. Wilcox, USDA, Chm. (1981)
Department of Agronomy
Purdue University
W. Lafayette, IN 47907

B) Organization of the Committee:

- 1) The Committee will be composed of six elected members and the editor of the Soybean Genetics Newsletter.
- 2) The term of the elected members will be three years. After a member has been off for one year, he (she) can be reelected. The Committee will elect two new members each year; a simple majority is needed for election. The members will be elected prior to February 1 of each year, by a mail ballot conducted by the chairman.
- 3) At the annual meeting of the Committee (usually in February in conjunction with the Soybean Breeding and Genetics Workshop), the two new members and the two retiring members of the Committee are eligible to attend and vote.
- 4) The Chairman will be elected at the annual Committee meeting and serve through the next annual meeting, and may be reelected.

C) The duties of this Committee include the following:

1) Maintain Genetic Collection.

The Genetic Collection is divided into four categories:

- a) Type Collection includes all published genes of soybeans, preferably in the original strains (excluding U.S. and Canadian name varieties, which are maintained in a separate collection) plus certain mutants or strains that appear to the Committee to have potential genetic interest.
- b) Isoline Collection includes adapted varieties Clark, Harosoy and Lee, into which have been backcrossed single genes or combinations of genes. Also included are certain genes or combinations with Chippewa, Wayne and Williams.
- c) Linkage Collection includes linkage combinations and the various genetic recombinations.
- d) Cytological Collection includes translocations, inversions, deficiencies, trisomics, tetraploids, etc.

Collections a, b and c are maintained at Urbana, Illinois, with R. L. Bernard as curator. Collection d is maintained at Ames, Iowa, with R. G. Palmer as curator.

2) Manuscript review and genetic symbol approval.

The Soybean Genetics Committee requests that researchers submit all manuscripts concerning qualitative genetic interpretation and symbols to the Committee Chairman. This review by the Genetics Committee will serve to insure orderly identification and use of genetic nomenclature and to avoid conflict of symbols. This will also allow assignment of type collection designations (T-numbers) prior to publication, so that these T-numbers may be used in the journal article to identify parental lines.

3) Soybean Genetics Newsletter notes.

All notes for the Newsletter should be sent to the SGN editor, R. G. Palmer, who will ask the Soybean Genetics Committee to review those articles concerning qualitative genetic interpretation and symbols. Genetic symbols reported in the Newsletter will have the same status as those published in scientific journals.

- D) The Committee will take the responsibility for publishing every five years, starting in 1981, in the SGN a list of all gene symbols, linkage groups, translocations, and trisomics in soybeans. Researchers who have references on the gene symbols and linkage groups are urged to send them to R. L. Bernard or T. Hymowitz. Researchers who have references on translocations and trisomics are urged to send them to R. G. Palmer.
- E) The function of the Committee was officially expanded to include genetics research in the entire Glycine genus rather than restricting its responsibilities to Glycine max.
- F) Researchers submitting manuscripts on new gene symbols are urged to furnish R. L. Bernard with seeds of the line carrying the reported gene. From 50 seeds to 300 gms of seed of each line are needed to maintain the genetic type collection. When these seeds are received, the genetic type number can be assigned and can then be reported by the author in a manuscript.

Rules for Genetic Symbols

I) Gene Symbols

- a) A gene symbol shall consist of a base of one to three letters, to which may be appended subscripts and/or superscripts as described below.
- b) Genes that are allelic shall be symbolized with the same base letter(s) so that each gene locus will be designated by a characteristic symbol base.
- c) The first pair of genes reported for a gene locus shall be differentiated by capitalizing the first letter of the symbol for the dominant or partially dominant allele. (Example: Ab, ab. Ab is allelic and dominant to ab.) If genes are equivalent, codominant, or if dominance is not consistent, the capitalized symbol may be assigned at the author's discretion.
- d) When more than two alleles exist for a locus, the additional alleles or those symbolized subsequently to the pair first published shall be differentiated by adding one or two uncapitalized letters as a superscript to the base. (Example: R, r^m, r.) This shall be the only use of superscripts. The base for the additional alleles is capitalized only when the gene is dominant or equivalent to the allele originally designated with a capitalized symbol. The superscript may be an abbreviation of a descriptive term. When allelism is discovered for a gene previously assigned a symbol, the previous symbol may be used as the superscript.
- e) Gene pairs with the same or similar effects (including duplicate, complementary, or polymeric genes) should be designated with the same letter base differentiated by numerical subscripts, assigning 1, 2, 3, 4, etc., consecutively in the order of publication. (Example: The y series for chlorophyll deficiency.) This shall be the only use of subscripts. Letter subscripts should not be used. The subscript 1 is automatically a part of the first reported gene symbol for each base but may be omitted until the second symbol is assigned.
- f) Base letters may be chosen so as to indicate apparent relationships among traits by using common initial letters for all loci in a related

group of traits. Examples are P for pubescence type, R for disease reaction (plus two initials of the pathogen to complete the base), and L for leaf shape.

- g) The distinction between traits that are to be symbolized with identical, similar, or with unrelated base letters is necessarily not clear cut. The decision for intermediate cases is at the discretion of the author but should be in accordance with previous practices for the particular type of trait. The following sections concern supplementary symbols that may be used whenever desired as aids to presentation of genetic formulas.
- h) A dash may be used in place of a gene symbol to represent any allele at the indicated locus. The locus represented should be apparent from its position in the formula. (Example: A _ represents both AA and Aa.)
- i) A question mark may be used in place of a symbol when the gene is unknown or doubtful, or it may be used as a superscript to the base symbol for the same purpose. (Example: a[?] indicates that the latter is an unknown allele at the A locus.)
- j) Plus symbols may be used in place of the assigned gene symbols of a designated standard homozygous strain when this will facilitate presenting genetic formulas. The standard strain may be any strain selected by the worker, as long as the strain being used and its genetic formula are made explicit.

II) Linkage and Chromosome Symbols

- a) Linkage groups and the corresponding chromosomes shall be designated with Arabic numerals. Linkage shall be indicated in a genetic formula by preceding the linked genes with the linkage group number and listing the gene symbols in the order that they occur on the chromosome.
- b) Permanent symbols for chromosomal aberrations shall include a symbol denoting the type of aberration plus the chromosome number(s) involved. Specific aberrations involving the same chromosome(s) shall be differentiated by a letter as follows: The symbol Tran shall denote translocations. Tran 1-2a would represent the first case of reciprocal translocations between chromosomes 1 and 2, Tran 1-2b the second, etc.

The symbol Def shall denote deficiencies, Inv inversions, and Tri primary trisomics. The first published deficiency in chromosome 1 shall be symbolized as Def 1a, the second as Def 1b, etc. The first published inversion in chromosome 1 shall be denoted as Inv 1a, etc. The first published primary trisomic shall be designated with the Arabic numeral that corresponds to its respective linkage group number.

- c) Temporary symbols for chromosomal aberrations are necessary, as it may be many years before they are located on their respective chromosomes. Tran 1 would represent the first case of a published reciprocal translocation; Tran 2, the second case, etc. The first published deficiency shall be symbolized as Def A, the second as Def B, etc. The first published inversion shall be symbolized as Inv A, the second as Inv B, etc. The first published primary trisomic shall be designated as Tri A, the second as Tri B, etc. When appropriate genetic and/or cytological evidence is available, the temporary symbols should be replaced with permanent symbols, with the approval of the Soybean Genetics Committee.

III) Cytoplasmic Factor Symbols

- a) Cytoplasmic factors shall be designated with one or more letters prefixed by cyt-. (Example: cyt-G indicates the cytoplasmic factor for maternal green cotyledons, cyt-Y indicates that for maternal yellow cotyledons.)

IV) Priority and Validity of Symbols

- a) A symbol shall be considered valid only when published in a recognized scientific journal, or when reported in the Soybean Genetics Newsletter, with conclusions adequately supported by data which establish the existence of the entity being symbolized. Publication should include an adequate description of the phenotype in biological terminology, including quantitative measurements wherever pertinent.
- b) In cases where different symbols have been assigned to the same factor, the symbol first published should be the accepted symbol, unless the original interpretation is shown to be incorrect, the symbol is not in accordance with these rules, or additional evidence shows that a change is necessary.

V) Rule Changes

- a) These rules may be revised or amended by a majority vote of the Soybean Genetics Committee.

IV. COMMITTEES NAMED BY SOYBEAN GENETICS COMMITTEE

Requests were received by the Soybean Genetics Committee to nominate candidates to serve on two committees that are concerned with soybean production research.

National Plant Genetic Resources Board

The National Plant Genetic Resources Board (NPGRB) requested three individuals in soybean research be designated as contact persons for soybean research. The NPGRB has responsibility for providing advice on national policies for soybeans. The individuals nominated to assist this board will serve only as contact people for the groups they represent. Individuals nominated are: T. Hymowitz for State Agricultural Experiment Stations; J. R. Wilcox for USDA-SEA; and H. B. Collins for private industry.

Soybean Germplasm Advisory Committee

This Committee was established at a meeting of the Soybean Genetics Committee at Ames, Iowa in March, 1979 in response to a generally believed need for a group which could function in the following ways:

- 1) To serve in an advisory capacity to the National Plant Germplasm Committee, to the Germplasm Resources Information Program, and to other national groups concerned with soybean germplasm.
- 2) To serve in an advisory capacity to the curators of the soybean germplasm collection and to promote and coordinate the worldwide procurement of soybean germplasm and programs concerning its maintenance, evaluation, and distribution.
- 3) To serve in an advisory capacity to research institutions, especially the USDA and the state agricultural universities, in fostering soybean germplasm programs.

The Committee consists of the curators and representatives of the evaluators and users of soybean germplasm. Current members in addition to curators E. E. Hartwig and R. L. Bernard are R. L. Nelson, USDA and University of Illinois, whose full-time assignment is germplasm evaluation and who is acting as chairman of the Committee; M. J. Sullivan, entomologist at Clemson University; S. M. Lim, USDA pathologist at the University of Illinois; C. W. Jennings,

breeder with Pioneer Hi-Bred International in Iowa; J. W. Lambert, breeder at the University of Minnesota; and C. Williams of Jacob Hartz Seed Company in Arkansas.

The Committee held its first meeting on February 19, 1980 in St. Louis, Missouri in conjunction with the national soybean breeders workshop. The organization, purpose, and functioning of the Committee was discussed, followed by a presentation of the Germplasm Resources Information Program by P. Callas and J. Scott of LISA, University of Colorado, and finally a discussion of the traits to be emphasized in soybean germplasm evaluation led by R. L. Nelson.

The Committee's procedures and policies are still in a formative state. The Committee has the option of meeting annually in conjunction with the annual soybean workshop, but since some of the members do not attend this meeting every year it was recommended that as much business as possible be conducted by mail. During the upcoming initial year of activity the Committee will function under the chairmanship of R. L. Nelson with assistance from the two curators. Approximately a year from now the Committee will consider the question of terms of office, election or selection of new members and officers, etc. Periodically it will assess the state of soybean germplasm and consider its inputs and where it might beneficially influence such matters. We invite all members of the soybean research community to convey to any Committee member any ideas they have concerning the Committee's area of interest.

R. L. Bernard
Research Geneticist

R. L. Nelson
Research Geneticist

V. USDA SOYBEAN GERMPLASM COLLECTION

The Collection has continued to grow during the past year with over 300 added to the available list for the Urbana collection and over 1500 new introductions (mostly from the Soviet Union) grown at Urbana in 1979. The decade from 1970 to 1979 has been a very active one with the following numbers of introductions received from the indicated countries of origin:

S. Korea	2338
USSR	1522 (incl. 762 originally from China)
Japan	1070
China	166
India	54
Taiwan	17
Other Asia	18 (Thailand, Pakistan, Nepal, Hong Kong)
Romania	143
Bulgaria	44
Other Europe	47 (Yugoslavia, Sweden, Poland, Hungary)
Uganda	29
Other Africa	28 (Nigeria, Rhodesia, S. Africa, Cameroun, Sierra Leone)
Other	<u>3</u> (Australia, Argentina, Brazil)
Total	5479

The exact number added to the Collection will differ from the above because of duplications, sublining, and inviable seeds.

A major project underway is the preparation of a complete numerical list of soybean introductions, their origin, foreign variety name, and our classification as to maturity group. This should be available in a few months and will be the first time such a list has been available outside of the annually published "Plant Inventory" which is cumbersome to use, since it includes all crops and lists what is introduced but not what is being maintained.

Plans have been made for the general agronomic evaluation of northern germplasm introduced after 1960 (PI numbers higher than 266,807) which includes all those not in the evaluation reports of 1965 to 1969. Tests of the 00 to IV germplasm will be conducted in 1980 with a second rep in 1981. The 363 entries of Groups 00 and 0 will be grown in Minnesota by Jean Lambert (a Group 000 will be split off), the 791 entries of late IV maturity will be grown at Lexington, Kentucky by James Orf, and the remaining 1616 entries (Groups I, II, III, and early IV) will be grown at Urbana, Illinois by Randall Nelson. As soon as chemical analyses of the seeds from the 1981 crop are completed, the data will

be compiled and reports made available, probably in early to mid-1982.

This renewed evaluation effort has been made possible by the establishment of the new USDA position at the University of Illinois emphasizing germplasm evaluation, utilization, and development and now occupied by R. L. Nelson. We are also especially indebted to Dr. Lambert at the University of Minnesota and Dr. Orf at the University of Kentucky for their willingness to devote a considerable amount of effort to germplasm evaluation.

Since some confusion has arisen, it should be pointed out that Nelson's assignment is the evaluation and utilization of germplasm. The maintenance and distribution of seeds is handled by the curators, Hartwig and Bernard, and requests for seeds should be addressed to them.

The germplasm lists and reports below are available from

Dr. R. L. Bernard, USDA
Turner Hall - Agronomy
University of Illinois
Urbana, IL 61801

Those marked with an asterisk are available from

Dr. E. E. Hartwig, USDA
Delta Branch Experiment Station
Stoneville, MS 38776

Checklists giving name and maturity group (extra copies available to use in making requests for large numbers of strains):

- 1) Checklist of U.S. and Canadian varieties (00 to IV), January 1980.
- 2) Checklist of FC and PI strains (00 to IV), January 1980.
- *3) Checklist of varieties and FC and PI strains (V to X).

Evaluation reports giving origin of strains and descriptive, agronomic, and seed composition data:

- 1) Varieties, Groups 00 to IV, 1970.
- 2) Varieties and FC and PI strains, Groups 00 to 0, 1965.
- 3) Varieties and FC and PI strains, Groups I to II, 1966.
- 4) Varieties and FC and PI strains, Groups III to IV, 1969.
- *5) Varieties and FC and PI strains, Groups V to X, 1975.
- 5) Recent additions, varieties and PI, Groups 00 to IV, 1970.

List of Genetic Type Collection, Feb. 1976 and additions to Aug. 1979.

List of backcross isolines of Clark and Harosoy, 1975 (1980 available soon).

List of wild soybeans, Glycine soja, 1976, and 1979 additions.

List of Perennial Glycine accessions, June 1979.

R. L. Bernard
Research Geneticist

R. L. Nelson
Research Geneticist

VI. RESEARCH NOTES

ALABAMA A&M UNIVERSITY
Department of Natural Resources
Normal, AL 35762

1) Evaluation of soybean germplasm for aluminum tolerance.

A growth-chamber experiment was conducted in nutrient solution containing 0 or 8 ppm of aluminum as $Al_2K(SO_4)_3$ to study differential Al tolerance of soybean germplasm representing Maturity Groups V, VI and VII, supplied by Dr. E. E. Hartwig. Two soybean cultivars, one sensitive ('Chief') and the other tolerant ('Perry'), were included as standard checks (Fig. 1).

Soybean roots were affected by the presence of Al and showed discoloration, stunted and blackish root tips. Abnormal leaf characteristics, such as narrow leaves, leaf chlorosis and short plant growth, were associated with high level of Al in nutrient solution. The average relative root length (8 ppm/0 ppm) of lines in Maturity Groups (MG) V, VI and VII was 34.5, 75.0 and 65.0%, respectively. The range of the relative root length was noticed from 18 to 179% in MG V, 24 to 200% in MG VI and 45 to 143% in MG VII. The relative root length of aluminum-tolerant Perry and aluminum-sensitive Chief was 130 and 50%, respectively.

Another measure of Al tolerance was studied by comparing the top and root dry weight of cultivars on the unlimed and limed Bladen clay loam soils in a greenhouse. The sensitive varieties (Chief, 'Essex', 'Ransom', 'Forrest') showed chlorosis of leaves of varying degrees. The symptoms were severe on the youngest leaves; the data on the relative root and top dry weight and root length of nine soybean cultivars are presented in Table 1.

Reference

Sapra, V. T., T. Mebrahtu and L. M. Mugwira. 1979. Evaluation of soybean germplasm Maturity Groups V, VI and VII for agronomic characters and aluminum tolerance. Special publication, Alabama A&M Univ., Normal, AL 35762 (paper presented at Southern Branch of American Society of Agronomy, Hot Springs, AR, Feb. 3-6, 1980).

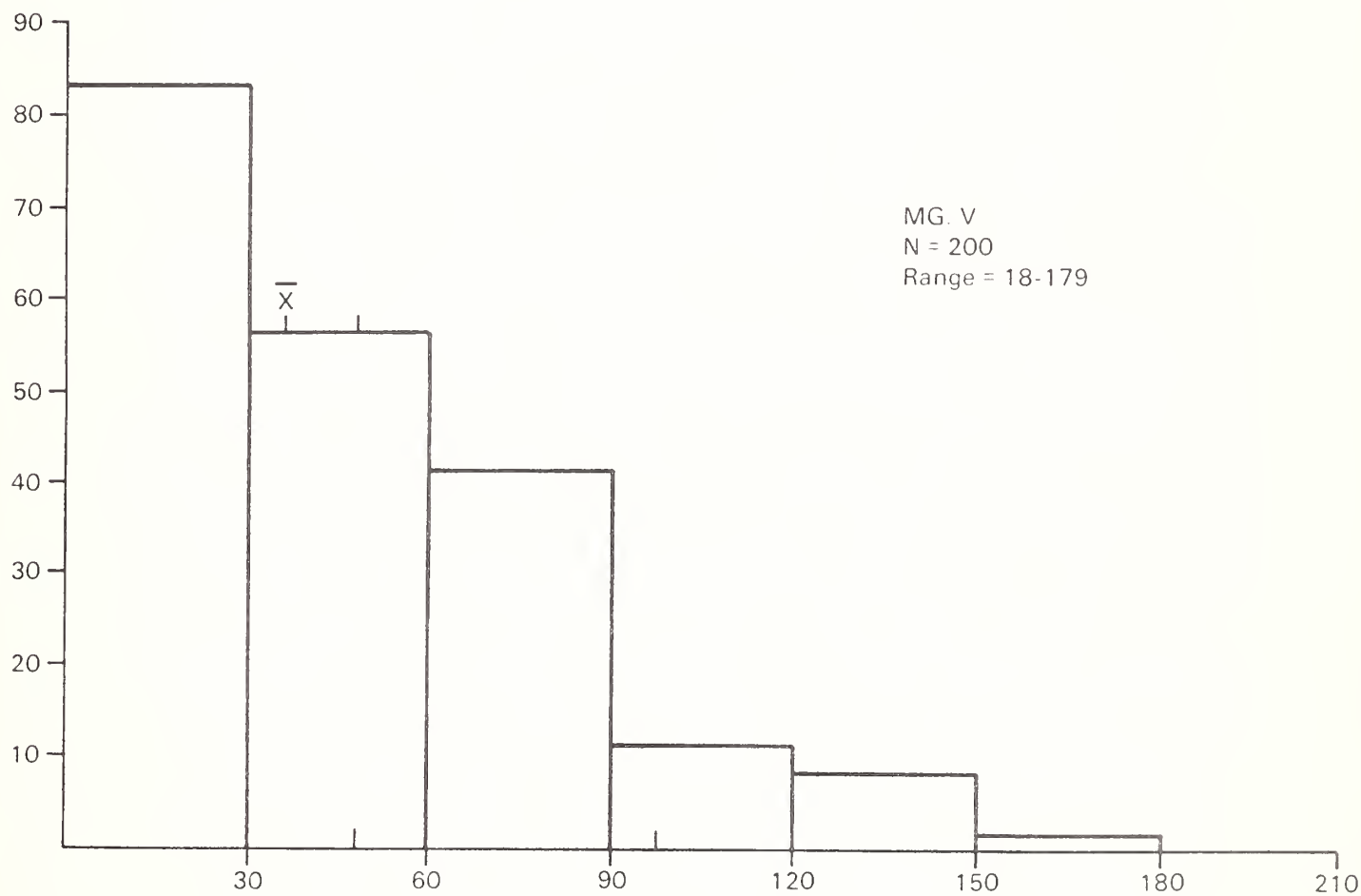
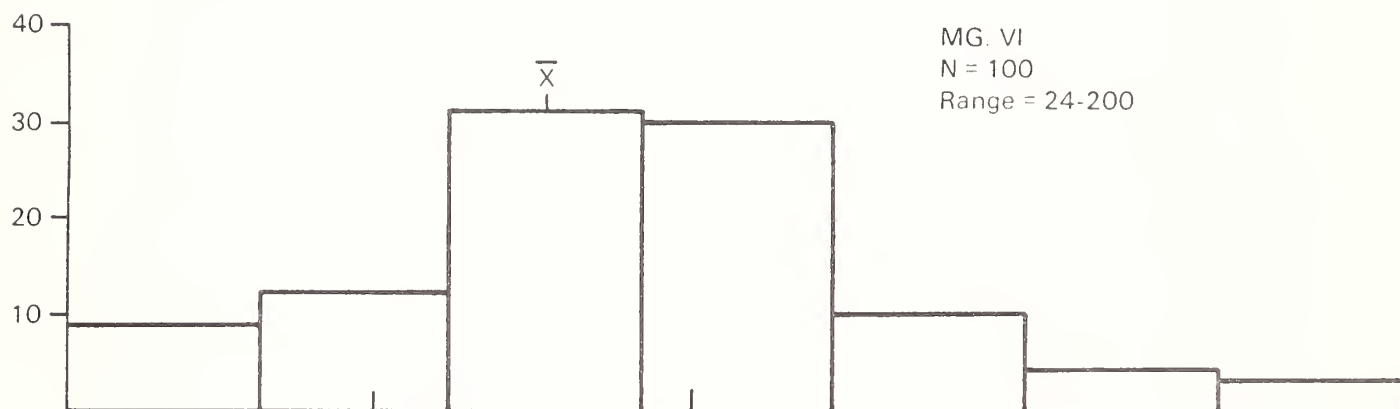
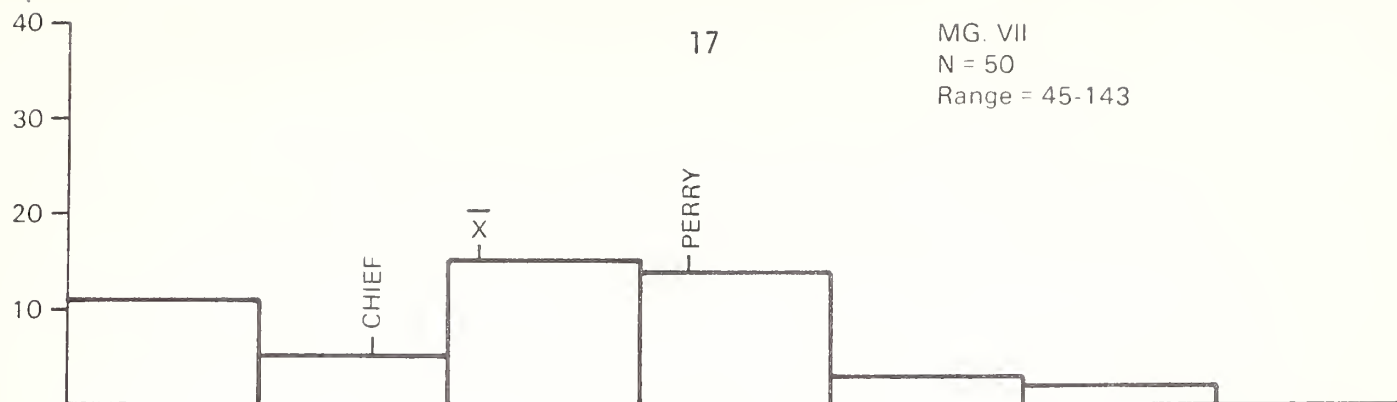


Figure 1. RELATIVE ROOT LENGTH (%)

Table 1
Relative root and top dry weight and root length
of nine soybean cultivars

Maturity Group	Cultivars	<u>Relative dry weight</u>		Relative root length ¹
		Root	Top	
VII	Ransom	0.73	0.78	0.65
V	Centennial	1.00	0.97	0.89
V	Essex	0.73	0.98	0.84
V	Forrest	0.75	0.78	0.67
V	Hill	1.04	1.04	0.32
V	York	0.96	0.98	0.96
VI	Lee	1.04	0.89	1.43
IV	Perry	1.20	1.12	1.30
IV	Chief	0.70	0.83	0.50

¹Data from nutrient solution study.

Val T. Saprà
Taddesse Mebrahtu
Luke M. Mugwira

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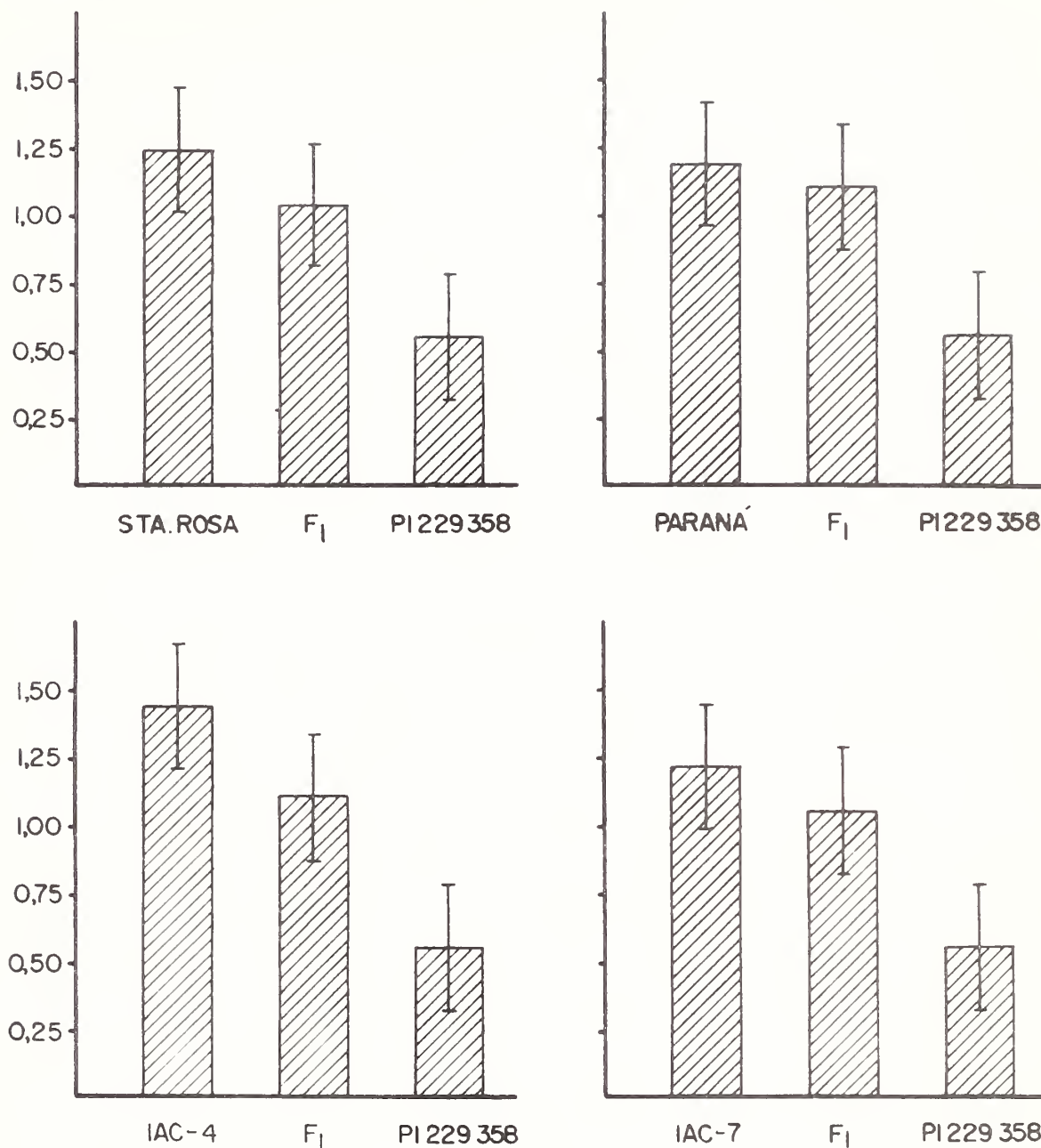
1) Oviposition of *Bemisia tabaci* (Genn.) in F₁ soybean plants of crosses
between PI 229,358 and commercial varieties.*

The whitefly *Bemisia tabaci* is an important vector of virus diseases of cotton, soybean, bean, tomato and other crops. Soybean is a good host for this insect and the increase in the soybean acreage in Brazil has brought an uprise in the whitefly population and whitefly-transmitted viruses.

The introduction of resistance against this whitefly in soybean commercial varieties may benefit many crops in Brazil.

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Log(10.eggs/cm²)



L.S.D. (Tukey 5%) = 0,460

C.V. = 24,00 %

Fig.1 Average oviposition of *Bemisia tabaci* on leaves of different soybean cultivars, the PI 229 358 and their F₁

The preference for oviposition of B. tabaci was studied in the parents and F₁ plants from crosses between the resistant PI 229,358 and the varieties 'Santa Rosa', 'Parana', IAC-4 and IAC-7. A free-choice type of experiment was conducted under greenhouse conditions, utilizing potted plants distributed in randomized blocks with 9 treatments and 7 replications.

Four days after artificial infestation with the adults, the number of eggs per cm² of leaves was estimated in samples of two trifoliolates per plant.

Figure 1 summarizes the results obtained. The PI 229,358, commercial varieties, and F₁ plants received respectively the least, the most and intermediate number of eggs.

Reference

Rossetto, D., A. S. Costa, M. A. C. Miranda, V. Nagai and E. Abramides. 1977. Differences in the oviposition of Bemisia tabaci in soybean varieties. An. Soc. Entomol. Bras. 6(2): 256-263. (In Portuguese with English summary).

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2) Performance of F_1 generation of soybean in relation to Colaspis sp. and Diabrotica speciosa.

Resistance against the leaf beetles Colaspis sp. (C. occidentalis or near occidentalis according to Dr. R. White, Insect Identification and Beneficial Insect Introduction Institute, Beltsville, MD, USA) and Diabrotica speciosa (Germar, 1824) were evaluated under greenhouse conditions, utilizing the resistant PI 227,687, two commercial susceptible varieties 'Santa Rosa' and 'Parana', and the two F_1 between the PI and these commercial varieties.

A free-choice type of test, with five replications, and artificial infestation of field-collected adults, was made and the percentage of leaf area eaten was visually estimated.

Tables 1 and 2 show the percentage of leaf area eaten by C. occidentalis and D. speciosa. The first species, C. occidentalis, showed preference to feed on old leaves over young leaves.

The F_1 generation performed as the resistant parent in relation to both species of beetles, which suggests a dominant type of resistance. This does not mean, however, that the same genetic factor is responsible for these resistances.

The number of petioles cut by D. speciosa (Table 2) is correlated positively with the percentage of leaf area eaten by this species.

Table 1
Percentage of leaf area eaten by Colaspis sp. in young and old leaves of soybean of different varieties

Treatment	% of leaf area eaten by adults*		
	Young leaves	Old leaves	Total
Parana	20,93 a	43,68 a	39,31 a
Santa Rosa	28,26 a	36,78 a	31,45 a
F_1 (S. Rosa x PI 227,687)	10,64 b	22,43 b	16,05 b
PI 227,687	11,32 b	18,55 b	13,62 b
F_1 (Parana x PI 227,687)	8,43 b	15,12 b	11,54 b
C.V. (%)	27,30	29,40	28,80

*Means followed by the same letter do not differ significantly by the Tukey test at 5% level.

Table 2
Percentage of leaf area eaten and number of petioles cut by
Diabrotica speciosa in soybean varieties

Treatment	Percentage of leaf area damaged*	Number of petioles cut*
Parana	52,83 a	1,44 a
Santa Rosa	52,25 a	1,46 a
F ₁ (Santa Rosa x PI 227,687)	10,52 b	0,91 b
F ₁ (Parana x PI 227,687)	6,00 b	0,71 b
PI 227,687	5,01 b	0,71 b
C.V. (%)	23,20	23,50

*Means followed by the same letter do not differ significantly by the Tukey test at the 5% level.

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1) Flavonol classes of cultivars in Maturity Groups 00-IV.

Since the complementary action of Fg₁ and Fg₃ in producing kaempferol 2^G-glucosyl-gentiobioside (Buttery and Buzzell, 1975) is associated with deleterious effects on chlorophyll concentration, photosynthetic rate and yield (Buttery and Buzzell, 1976), the bringing together of these two genes in crosses may necessitate selection against the Fg₁-Fg₃-genotype in the segregating material. For example, with the cross of 'Corsoy' (Fg₁ fg₃) x 'Hawkeye' (fg₁ Fg₃) at Iowa State University, visual selection was carried out against "chlorophyll deficient" types during inbreeding in order to develop lines for a physiological study. At the time of selection it was not known that flavonol-glycoside genes were involved. Advanced lines were later classified using thin layer chromatography (Buttery and Buzzell, 1973). The distribution

of the eight flavonol classes, which should occur in approximately equal numbers, was as follows:

<u>Class</u>	<u>No. of lines</u>
1t	14
2t	15
3t	2
4t	13
5t	12
6t	14
7t	13
8t	9

Thus, visual selection was effective in eliminating most of the 3t lines but had little effect on the frequency of 1t lines. The use of a portable photometer (Macnicol et al., 1976) might make it possible to easily select against the 1t class. For example, average readings of 442, 445, and 485 (indicating increasing chlorophyll concentration) were obtained with such a "chlorophyll meter" for one 3t line, 13 1t lines, and 12 7t lines, respectively, from the above cross in 1979. However, data have not been obtained on the variation in chlorophyll concentration across the eight flavonol classes; we are developing isoline sets for 1t-8t which should allow us to make these determinations.

The opposite approach to selection against the Fg₁ Fg₃ combination is to plan crosses so that whenever possible Fg₁ and Fg₃ are not brought together. Thus, it would be desirable to develop disease-resistant lines, male-sterile lines, and other lines which are to be used frequently in crosses as fg₁ fg₃ genotypes. Varieties developed by hybridization, along with parental lines/varieties, are listed by Fg₁ Fg₃ genotype and flavonol class in Table 1 for Maturity Groups 00-IV. The approximate gene frequencies for Fg₁ and Fg₃ in this germplasm pool of 112 varieties/lines are 0.09 and 0.40, respectively. These frequencies are similar to the 0.10 and 0.28 reported by Buttery and Buzzell (1976) for 78 of these varieties.

Table 1

Flavonol classification of North American public soybean cultivars
(Maturity Groups 00-IV) developed by hybridization and
released from 1937 through 1976, plus parental lines/varieties

Class	Variety	Class	Variety
<u>Cultivars with Fg₁ Fg₃</u>			
1T	Nil	1t	Nil
3T	Nil	3t	Nil
<u>Cultivars with Fg₁ fg₃</u>			
2T	Provar	2t	AK (Harrow) Amsoy Chief Corsoy Evans Harcor Harosoy [†] Illini Wilkin
5T	Nil	5t	Nil
<u>Cultivars with fg₁ Fg₃</u>			
4T	Flambeau Norchief Sac Swift Vansoy Wye C799 C1069 L49-4091 M372	4t	Adelphia Aoda Bethel Delmar HP-963 Jogun Kanro Kim Magna Morsoy Mukden Patoka Perry Prize Protana Renville Scott C1266R FC33243 L37-1355 L46-5679

Table 1 (cont'd)

Class	Variety	Class	Variety
<u>Cultivars with fg₁ Fg₃ (cont'd)</u>			
7T	Manitoba Brown Midwest	7t	Blackhawk Clay Disoy Goldsoy Hark Hawkeye Kanrich Richland Seneca Verde L48-7289
<u>Cultivars with fg₁ fg₃</u>			
6T	Altona Capital Clark Columbus Cutler Ford Kent Lincoln Mansoy Maple Arrow Pomona Shelby Viking Wayne Williams Woodworth C1270 052-903	6t	Acme Ada Adams Bonus Coles Comet Crest Dunfield Gibson Hardome Harosoy [†] Harwood Hodgson Lindarin Madison Mandarin (Ott.) Merit Norman Pagoda Portage Steele Traverse Wabash Wells C1265 L57-0034 L59-738 OX383

Table 1 (cont'd)

Class	Variety	Class	Variety
<u>Cultivars with fg₁ fg₃ (cont'd)</u>			
8T	Calland Chippewa Dunn Grant Rampage Ross Wirth 840-7-3	8t	Beeson Harlon Harly Henry Monroe

[†]Variety is heterogeneous for two classes; in many of the varieties/lines, only a single plant was tested as being representative of the variety/line.

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1) Inheritance of insensitivity to long daylength.

Genetic tests for daylength insensitivity have been run using PI 297,550, reported to be day-neutral by Polson (1972), as source material. Segregating material was grown under long days at various times from 1973 to 1979, either in a growth cabinet (Buzzell et al., 1974) or in a greenhouse with daylength

extended to 20 hours with incandescent light. Material was classified at 35 to 42 days after planting as either non-flowering, sensitive (S), or flowering, insensitive (I).

The results gave a good fit to expected ratios for a single recessive gene controlling insensitivity (Table 1). Results for an insensitive line, OX619, grown in the field at Harrow and under various daylengths at Ottawa, are given in Tables 2 and 3, respectively.

Table 1
Segregation for sensitive (S) and insensitive (I) responses under
20 hr daylength (non-flowering and flowering
at 35-42 days after planting)

Cross*	F ₂			F ₃		
	S	I	χ^2 3:1	S	Seg.	I
PI 297,550 (I) x OX301 (S)	43	15	0.023	13	23	9
OX637 (I) x Harcor (S)	13	3	0.333	5	8	3
OX633 (I) x OX318 (S)	60	21	0.037	-	-	-
Pooled	116	39	0.009	18	31	12 [†]

*PI 297,550, Group 00, from Hungary; OX301 from OX250 (Blackhawk x Midwest) x OX383 (Corsoy x Harosoy 63); OX637 from PI 297,550 x OX301; Harcor from OX383 x Corsoy; OX633 from OX637 x Harcor; and OX318 from OX383 x OX384 (a sister line of OX383 but earlier maturing).

[†] χ^2 for 1:2:1 is 1.197, P = 0.70 - 0.50.

Bernard (1971) has characterized maturity genes $\underline{E}_1/\underline{e}_1$ and $\underline{E}_2/\underline{e}_2$, and Buzzell (1974) has reported $\underline{E}_3/\underline{e}_3$. The observed daylength-incandescent response seems sufficiently different from that of the previously reported genes to obviate the need for allelism tests. Gene symbols $\underline{E}_4/\underline{e}_4$ are proposed. Determining the linkage groups of the "E" genes in the future ($\underline{E}_1/\underline{e}_1$ is in linkage group 1, Weiss 1970) should establish definitely whether or not allelism is involved. $\underline{E}_4/\underline{e}_4$ is not linked with $\underline{Fg}_1/\underline{fg}_1$ (Buzzell, 1978. Linkage has not been demonstrated for $\underline{E}_3/\underline{e}_3$ (Buzzell, 1974; 1975).

Table 2

Field comparison of OX619 (OX633 x OX318), which is insensitive to long (20 hr) daylength, with other material planted June 7, 1979 at Harrow

Line	Days from emergence (June 12) to:			Plant height cm
	50% flowering flowering	R5*	Maturity	
OX619	41	56	93	68
OX633	45	58	99	80
OX637	45	58	93	72
OX318	44	61	107	60
Harcor	53	71	116	97
Harosoy \underline{e}_3	44	60	104	92
Harosoy \underline{E}_3	49	68	109	90
L.S.D. 0.05	1.4	0.9	3.4	8.5
0.01	1.9	1.2	4.6	11.4
C.V. %	2	1	4	7

* Beans just beginning to be felt in the pod.

Other genes are involved in insensitivity to long daylength; for example, the F_2 of OX619 x OX328E (early-maturing line from 'Harosoy' x 'Woodworth') segregated 56 non-flowering : 4 flowering which gives a good fit to a 15:1 ratio for two genes. And, with OX619 under extended daylength at Ottawa and Harrow, flowering and pod development are both insensitive to long daylength in contrast to some other material which may flower early but is delayed in pod development (unpublished results). We are continuing research to classify the genes involved.

Table 3

Response of OX619 to various daylengths in comparison to insensitive and sensitive varieties; growth cabinet, Ottawa 1979

Variety	Stage	Days from emergence at			
		12 hr	16 hr	20 hr	24 hr
OX619	Flowering	27	30	29	36
	R4	38	36	37	43
Maple Presto*	Flowering	24	27	31	33
	R4	35	36	37	42
Harosoy e_3	Flowering	28	29	40	56
	R4	35	39	54	73

* Maturity Group 000 variety adapted to about 50°N in Canada.

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1) Increasing phytophthora-rot severity in field screening.

Walters and Caviness (1968) reported that phytophthora-susceptible varieties in Arkansas were more prone to the disease than resistant varieties if sprayed with 2,4-DB at flowering time. This increase in disease severity suggests that 2,4-DB could be used to increase the effectiveness of natural and mass selection (cf. Buzzell and Haas, 1972) for disease resistance/tolerance to Phytophthora megasperma var. sojae (Pms).

A non-replicated observation test was established in a field known to be infested with Pms races 3, 7 and 9 (T. R. Anderson, unpublished results) at the Soils Substation, Woodslee, Ontario. There were four bordered four-row strips in the field with each of the 16 rows being a different variety; each strip contained at least one susceptible, one tolerant, and one resistant variety. Plots (12 m long and four rows wide) were staked in four ranges; diseased plants in each plot row were counted and removed on July 31, 1979. Treatments (check, 0.06 and 0.24 kg 2,4-DB/ha) were applied August 1 using a hand-held, small-plot sprayer pressurized with CO₂ to 200 kPa and set to deliver 375 L H₂O/ha; randomization was restricted so that each treatment occurred once in each strip and each range. In addition, BASF 9052 grass-killer was applied with the 2,4-DB to some of the plots but it did not seem to influence the soybean response to Pms.

The average level of disease for susceptible, tolerant, and resistant varieties was fairly similar prior to treatment (Table 1). The 2,4-DB at 0.06 kg/ha increased the prevalence of disease considerably in susceptible varieties and somewhat in tolerant varieties. The 0.24 kg/ha rate markedly increased disease in both susceptible and tolerant varieties. The resistant varieties were not affected.

In field screening of bulk populations segregating for resistance/tolerance in Pms, a higher rate of 2,4-DB appears desirable for material segregating for resistance, a lower rate appears better for material segregating for tolerance. Natural/mass selection in such a nursery would probably entail some selection for herbicide tolerance to 2,4-DB since Pms-tolerant/resistant varieties appeared to differ in their degree of herbicide susceptibility to the 2,4-DB. 'Toyosuzu' was quite susceptible; later-maturing varieties like

Table 1
Phytophthora rot in soybeans treated
with 2,4-DB (Woodslee, 1979)

2,4-DB* kg/ha	Varieties	No. of diseased plants/ha	
		Emergence to July 31	Aug. 1 to Sept. 6
0.00 [†]	S	12,100	22,900
	T	400	2,500
	R	0	0
0.06 [†]	S	14,200	47,100
	T	800	7,100
	R	0	0
0.24	S	15,000	81,700
	T	1,200	56,300
	R	0	0

*Applied August 1.

[†]BAS 9052 post-emergent grass-killer applied at 0.60 kg/ha.

S = Beeson, Harosoy, Harwood, Wells.

T = Coles, Harcor, Jilin #8, Woodworth.

R = Toyosuzu, resistant to races 1-9; Beeson 80, Corsoy 79, Wells II, resistant to races 1-3, 6-9.

'Woodworth' were more susceptible than earlier-maturing ones; 'Coles' and 'Jilin #8' appeared to be fairly tolerant. Wax et al. (1974) reported that variety tolerance to 2,4-DB may be associated with tolerance to other herbicides such as bentazon.

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1) Photoperiodic response of wild soybeans collected from localities of different latitude in China.

In 1963, 16 wild soybeans (Glycine soja Sieb. and Zucc.) and 4 semi-cultivated soybeans (Glycine max (L.) Merr.) were collected from localities of different latitude in China (Table 1). They were tested under different photoperiods for their photoperiodic response. The experimental results are shown in Table 2. From the experimental data in Table 2 we can clearly see that wild soybeans collected from Yongtze River Valley ($30^{\circ}18'$ - $31^{\circ}54'$) and south region of China ($26^{\circ}56'$) are typical short-day plants. The nature of short day of the wild soybeans becomes weaker as their original regions move to the higher latitude. Wild soybeans collected from north part of Heilungkiang Province ($47^{\circ}20'$ - $48^{\circ}0'$) can flower and even mature under continuous day-length. The regular geographical distribution of such eco-types is due to the long-term natural selection of daylength of different latitudes during the growing season. The results also reveal that the short-day response of the wild soybeans is always stronger than the small-seeded semi-cultivated soybeans (Label No. 7, 17, 16, 20) (also cultivated types, Wang et al., 1956) of the same locality. This denotes that the nature of strong short-day response is a primitive character. Soybeans with weak short-day response (early in maturity) were derived from those with strong short-day response (late in maturity), and migrated gradually from south (low latitude) to north (high latitude). Based on such assumption, and the evidence of the unearthed crop grains of an ancient grave about 5,000 years ago in Zhejiang Province, we postulate that cultivated soybeans might originate from Yongtze River Valley or regions south of it.

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Table 1
Origin of the collected wild and semi-cultivated soybeans (1963)

Label no.	Materials	Locality of collection	Latitude of collection	Natural conditions of the locality			
				Daylength on summer solstice (hr:min.)	July mean temp. (°C)	Late frost (Month & day)	Early frost (Month & day)
4	Wild soy-bean	Fuyen, Heilungkiang	48°0'	16:0	22.1	May 14	Sept. 24
1	"	Chichi-har, Heilungkiang	47°20'	16:0	23.0	May 2	Sept. 22
2	"	Sweilin, Heilungkiang	47°20'	16:0	21.3	May 10	Sept. 20
3	"	Harbin	45°45'	15:54	23.3	May 5	Sept. 25
5	"	Changchun	44°0'	15:40	23.5	May 2	Sept. 27
6	"	Kungchulin, Chilin	43°30'	15:25	24.1	May 2	Sept. 25
8	"	Shenyung	41°47'	15:18	24.9	Apr. 29	Oct. 4
9	"	Dandun, Liaonin	40°30'	15:15	25.0	---	---
10	"	Beijing	39°57'	15:10	26.1	Mar. 24	Oct. 5
12	"	Delta of Yellow River	36°40'	14:54	28.4	Mar. 16	Nov. 5
13	"	Shaochinhe, Shantung	36°40'	14:54	28.3	---	---
11	"	Liangshan, Shantung	36°12'	14:35	28.0	---	---
18	"	Hafi, Anhui	31°54'	14:18	28.7	Mar. 13	Nov. 15
15	"	Wuhan	30°32'	14:10	29.6	Mar. 20	Nov. 8
14	"	Jingchou, Hubei	30°18'	14:8	27.1	---	---
19	"	Hungyong, Hunan	26°56'	13:42	29.1	Mar. 6	Dec. 16
7	Semi-cultivated	Kungchulin, Chilin	43°30'	15:25	24.1	May 2	Sept. 25
17	"	Hafi, Anhui	31°54'	14:18	28.7	Mar. 13	Nov. 15
16	"	Wuhan	30°32'	14:10	29.6	Mar. 20	Nov. 8
20	"	Changsa, Hunan	28°12'	13:50	30.0	Mar. 12	Nov. 8

Table 2

Experimental data of photoperiodic response of wild and semi-cultivated soybeans collected from localities of different latitude in China (1964-1965)

Label no. of collection	Latitude of collection	Daylength (hr)						
		10*	12	13.5	15	Natural daylength	18	Continuous light
4	48°0'	49	49 [†] (96)	50 (106)	55 (103)	60 (111)	75 (124)	97 (not)
1	47°20'	46	51 (103)	52 (114)	63 (106)	75 (129)	82 (127)	85 (137)
2	47°20'	48	52 (118)	54 (110)	65 (118)	83 (129)	87 (not) ^{††}	93 (not)
3	45°45'	47	49 (118)	58 (98)	67 (124)	85 (132)	90 (not)	107 (not)
5	44°0'	48	53 (104)	60 (93)	64 (129)	91 (133)	99 (not)	112 (not)
6	43°30'	49	54 (103)	59 (96)	75 (132)	101 (134)	113 (not)	106 (not)
8	41°47'	47	52 (118)	62 (104)	84 (not)	113 (not)	NB ^{†††}	NB
9	40°30'	45	55 (106)	63 (98)	93 (not)	109 (not)	NB	NB
10	39°57'	49	56 (88)	63 (103)	115 (not)	NB	NB	NB
12	36°40'	47	57 (104)	66 (114)	NB	NB	NB	NB
13	36°40'	46	54 (93)	64 (105)	NB	NB	NB	NB
11	36°12'	46	55 (93)	63 (107)	118	NB	NB	NB
18	31°54'	48	64 (118)	102 (not)	NB	NB	NB	NB
15	30°32'	48	65 (121)	93 (not)	NB	NB	NB	NB
14	30°18'	48	65 (119)	98 (not)	NB	NB	NB	NB
19	26°56'	49	65 (118)	96 (not)	NB	NB	NB	NB

35
Table 2 (cont'd)

Label no. of collection	Latitude of collection	Daylength (hr)						Continuous light
		10*	12	13.5	15	Natural daylength	18	
7	43°30'	48	54 (118)	58 (106)	65 (129)	87 (not)	94 (not)	NB
17	31°54'	48	62 (114)	91 (not)	NB	NB	NB	NB
16	30°32'	49	65 (118)	84 (not)	NB	NB	NB	NB
20	28°12'	49	60 (138)	91 (not)	NB	NB	NB	NB

* Results of 1965.

† Figures within parentheses are days from seeding to maturity; outside of them are days to flowering.

†† Not mature.

††† NB = no blooming.

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1) Seed acid phosphatase genotypes of cultivars in the USDA soybean collection.

Soybeans have three cultivar-specific electrophoretic forms of a seed acid phosphatase (Gorman and Kiang, 1977). Hildebrand et al. (1980) reported that the three acid phosphatase forms are inherited as codominant alleles at a single locus. The symbol Ap^a was assigned to the slow form, Ap^b to the intermediate and Ap^c to the fast form.

Seed of the cultivars screened for acid phosphatase forms were obtained from R. L. Bernard, USDA, Urbana, IL 61801 and E. E. Hartwig, USDA, Stoneville, MS 38776. The acid phosphatase genotypes of the soybean cultivars (Tables 1 and 2) were determined by a polyacrylamide gel electrophoretic procedure described by Hildebrand et al. (1980).

Table 1

Acid phosphatase form of named cultivars of the Northern U.S.
(Maturity Group 00 through IV)

Cultivar	Maturity group	Ap*	Cultivar	Maturity group	Ap*
Acme	00	B	Clark	IV	B
Ada	00	B	Clark 63	IV	B
Adams	III	B	Clay	0	B
Adelphia	III	B	Cloud	III	B
Agate	00	B	Columbia	III	B
AK (FC 30 761)	IV	B	Columbus	IV	B
AK Harrow	III	B	Comet	0	B
AK Kansas	IV	B	Corsoy	II	B
Aksarben	II	B	Crest	00	B
Altona	00	B	Custer	IV	B
Amsoy	II	B	Cutler	IV	B
Amsoy 71	II	B	Cutler 71	IV	B
Anoka	I	B	Cypress No. 1	IV	B
Aoda	IV	B	Delmar	IV	B
A-100	I	B	Disoy	I	B
Bansei Ames	II	B	Dunfield	III	C
Bavender Special A	III	C	Dunn	I	B
Bavender Special B	III	C	Early White Eyebrow	0	B
Bavender Special C	III	C	Earlyana	I	B
Beeson	II	B	Ebony	IV	A
Bethel	IV	B	Elton	I	B
Black Eyebrow	II	B	Emperor	IV	B
Blackhawk	I	B	Ennis I	III	B
Bonus	IV	B	Etum	II	B
Boone	IV	B	Evans	0	B
Burwell	I	B	Fabulin	IV	B
Calland	III	B	Flambeau	00	B
Capital	0	B	Ford	III	B
Carlin	IV	B	Fuji	III	B
Cayuga	I	B	Funk Delicious	IV	B
Chestnut	III	B	Funman	II	C
Chief	IV	B	Giant Green	I	B
Chippewa	I	B	Gibson	IV	B
Chippewa 64	I	B	Goku	II	B
Chusei	III	B	Goldsoy	0	B

Table 1 (cont'd)

Cultivar	Maturity group	Ap*	Cultivar	Maturity group	Ap*
Granger	III	B	Kingwa	IV	B
Grant	0	B	Kura	III	B
Green and Black	IV	B	Lincoln	III	B
Guelph	III	B	Lindarin	II	B
Habaro	I	B	Lindarin 63	II	B
Hahto Michigan	IV	C	Linman 553	II	C
Hakote	II	B	Little Wonder	III	B
Harbinsoy	IV	B	Macoupin	IV	B
Harcor	II	B	Madison	II	B
Hardome	0	B	Magna	II	B
Hark	I	B	Manchu	III	C
Harly	I	B	Manchu Lafayette	III	C
Harman	III	B	Manchu Lafayette B	III	C
Harosoy	II	B	Manchu Madison	II	C
Harosoy 63	II	B	Manchu Hudson	II	C
Hawkeye	II	B	Manchu Montreal	I	C
Hawkeye 63	II	B	Manchu 3 Wisc	II	C
Henry	II	B	Manchu 606 Wisc	II	C
Hidatsa	00	B	Manchukota	II	C
Higan	IV	B	Manchuria	I	B
Hodgson	I	B	Manchuria 13177	III	B
Hokkaido	IV	B	Manchuria 20173	III	B
Hongkong	IV	B	Mandarin	I	B
Hoosier	I	C	Mandarin Ottawa	0	B
HP-963	IV	B	Mandarin 507	I	B
Hurrelbrink	IV	B	Mandell	III	C
Illington	IV	B	Manitoba Brown	00	B
Illini	III	B	Mansoy	III	C
Ilsoy	III	B	Medium Green	I	B
Imperial	IV	B	Mendota	I	B
Jefferson	IV	B	Merit	0	B
Jogun	III	B	Midwest	IV	B
Jogun Ames	III	B	Miller 67	III	B
Kabott	0	B	Mingo	III	C
Kagon	I	B	Minsoy	00	B
Kanrich	III	B	Monroe	I	B
Kanro	II	B	Morse	IV	B
Kanum	II	B	Morsoy	00	B
Kent	IV	B	Mukden	II	B
Kingston	IV	B	Norchief	0	B

Table 1 (cont'd)

Cultivar	Maturity group	Ap*	Cultivar	Maturity group	Ap*
Norman	00	B	Sooty	IV	B
Norredo	IV	B	Sousei	II	B
Norsoy	I	B	Soysota	I	B
Ogemaw	00	B	Steele	I	B
Oksoy	IV	B	Swift	0	B
Ontario	I	B	Tastee	II	B
Osaya	III	B	Toku	II	A
Ottawa	I	B	Tortoise Egg	I	B
Pagoda	00	B	Traverse	0	B
Pando	00	B	Union	IV	B
Patoka	IV	B	Vansoy	0	C
Patterson	IV	C	Verde	III	B
Peking	IV	B	Viking	III	B
Pennsoy	III	C	Wabash	IV	B
Perry	IV	B	Wayne	III	B
Poland Yellow	0	B	Wea	II	B
Polysoy	IV	B	Wells	II	B
Portage	00	B	Wilkin	0	B
Portugal	I	B	Williams	III	B
Pridesoy 57	I	B	Willomi	III	B
Prize	II	B	Willomi B	III	B
Protana	II	B	Wilson	IV	B
Provar	II	B	Wilson B	III	B
Rampage	I	B	Wilson 5	IV	B
Renville	I	B	Wilson 5B	IV	B
Richland	II	B	Wilson 6	IV	B
Ross	III	B	Wing Jet	III	B
Sac	I	B	Wirth	I	B
Sanga	IV	B	Wisconsin Black	I	C
Sato-3	IV	B	Wolverine	III	B
Scioto	IV	C	Woodworth	III	B
Seneca	II	B	Wye	IV	B
Shelby	III	B	Yellow Marvel	II	B
Shingto	III	B			
Shiro	IV	B			

* A = Ap^a electrophoretic form at Rf 0.38; B = Ap^b electrophoretic form at Rf 0.42; C = Ap^c electrophoretic form at Rf 0.47. The Rf values of the three electrophoretic forms of acid phosphatase are relative to the Kunitz trypsin inhibitor (Ti^a) in a 10% polyacrylamide gel anodic system using pH 7.0 gel and bath buffers.

Table 2

Acid phosphatase form of named cultivars of the Southern U.S.
(Maturity Group V through IX)

Cultivar	Maturity group	Ap*	Cultivar	Maturity group	Ap*
Acadian	VIII	B	Hollybrook	V	B
Armredo	VI	B	Hood	VI	B
Arisoy	VIII	B	Hutton	VIII	B
Arksoy	VIII	B	Improved Pelican	VIII	B
Avoyelles	VIII	B	Jackson	VII	B
Barchet	VIII	B	JEW 45	VIII	B
Biloxi	VIII	B	Jupiter	IX	B
Bossier	VII	B	Kino	VI	B
Bragg	VII	B	La Green	VIII	B
Charlee	VII	B	Laredo	VI	B
Cherokee	VIII	B	Lee	VI	B
Clemson	VII	B	Lee	VI	B
Cobb	VIII	B	Lee 68	VI	B
Coker 338	VIII	B	Lee 74	VI	B
Coker Hampton	VIII	B	Luthy	V	C
Creole	VII	B	Mack	V	B
Dare	V	B	Magnolia	VI	B
Davis	VI	B	Majos	VIII	B
Delsoy	VI	B	Mammoth Yellow	VII	B
Delsta	VIII	B	Mamloxi	VIII	B
Dixie	V	B	Mamredo	VI	B
Dortchsoy 67	VII	B	Manotan 6640	VIII	B
Dyer	V	B	Misoy	VII	B
Easycook	VI	B	Monetta	VII	B
Essex	V	B	Nanda	VIII	B
Forrest	V	B	Nansemond	V	B
Gatan	VII	B	Nela	VIII	B
Georgian	VII	B	Old Dominion	VI	B
Haberlandt	VI	A	Otootan	VIII	B
Hampton 262	VIII	B	Palmetto	VII	B
Hampton 266A	VIII	B	Peking	IV	B
Hardee	VIII	B	Pickett	VI	B
Harrel	V	B	Pickett 71	VI	B
Hayseed	VI	B	Pine Dell Perfection	VI	B
Hinn	VI	B	Pluto	VII	B

Table 2 (cont'd)

Cultivar	Maturity group	Ap*	Cultivar	Maturity group	Ap*
Pochahontas	VII	B	Tarheel Black	VII	B
Ral soy	VI	B	Tenn Non-Pop	VII	B
Roanoke	VII	B	Tokyo	VII	B
Rokuson	VI	B	Tracy	VI	B
Rose Non-Pop	VI	B	Virginia-S	V	B
S-100	V	B	Volstate	VII	B
Semmes	VII	B	White Biloxi	VIII	B
Seminole	VIII	B	Woods Yellow	VII	B
Stuart	VIII	B	Yelrarda	VIII	B
Tanner	VII	B	Yelredo	VIII	B
			York	V	B

*A = Ap^a electrophoretic form at Rf 0.38; B = Ap^b electrophoretic form at Rf 0.42; C = Ap^c electrophoretic form at Rf 0.47. The Rf values of the three electrophoretic forms of acid phosphatase are relative to the Kunitz trypsin inhibitor (Ti^a) in a 10% polyacrylamide gel anodic system using pH 7.0 gel and bath buffers.

A note of caution: From a plant breeder's viewpoint the cultivar seed obtained from Drs. Bernard and Hartwig generally are pure. That is, the flower color, pod color, hilum color, etc., of each cultivar is uniform. However, from a biochemist's viewpoint the seed may be mixed. There are three possible sources for the mixtures: (1) The original parental lines may have had different allelic forms. By the time a cultivar is released it has been selfed for several generations and hence very few, if any, heterozygous seed can be found in a sample seed lot. (2) Natural outcrossing or mutations may have taken place during the multiplication process. And (3) during the harvesting and cleaning process alien seed may have been mixed in accidentally with the cultivar. Most frequently, the first two sources are the causes of a cultivar mixture. Therefore, we suggest that, when a new cultivar is to be categorized for a particular biochemical allele, at least 100 seed be tested. The seed tested should be breeders or foundation seed. In addition, the parental lines should be tested. It is important to determine whether the mixture is inherent in the cultivar or whether the mixture is due to some other cause. There is nothing intrinsically wrong with a cultivar that contains an inherent

mixture or mixtures of biochemical alleles; e.g., 'Cutler 71' and 'Williams 79' are mixtures of Ep and ep. Common sense must prevail and such cultivars should not be disqualified by either seed standard or certification agencies because they are "mixed".

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2) Screening the USDA soybean germplasm collections for lines lacking the 120,000 dalton seed lectin.

Pull et al. (1978b) screened 102 lines of soybeans [Glycine max (L.) Merr.] and found 5 lines lacking the 120,000 dalton seed lectin ('Columbia', 'Norredo', 'Sooty', 'T102', and 'Wilson-5'). The amount of soybean lectin (SBL) per g defatted meal and the amount of SBL content in soybean protein for the 102 lines tested also was published by Pull et al. (1978a). Orf et al. (1978) demonstrated, using polyacrylamide gel electrophoresis, that the presence of SBL is controlled by a single dominant gene designated Le. The homozygous recessive le le results in the lack of SBL.

The conventional Ouchterlony (1948) double diffusion technique was used in this study to screen for the presence or absence of SBL. Anti-serum with antibodies specific to SBL was obtained by immunizing adult male New Zealand white rabbits with purified soybean lectin and Freund's complete adjuvant emulsion (Orf, 1979). Twenty-four lines simultaneously were screened in each Ouchterlony plate (1% agar in 0.1 M pH 8.0 phosphate buffer). Ten μ l of seed extract (one seed ground in 2 ml of 0.092 M Tris and 0.023 M $\text{CaCl}_2 \cdot 2\text{H}_2\text{O}$ plus 1 ml of 0.4 g of sucrose per ml adjusted to pH 8.1) was pipetted into a well surrounding a central well containing 10 μ l of antiserum. Failure of a precipitin band to form indicated no detectable SBL present. Lines of G. max not showing lectin by this procedure were checked using polyacrylamide gel electrophoresis (Orf et al., 1978). In all cases the two procedures were in agreement.

The seed used in this study were obtained from R. L. Bernard, USDA, Urbana, IL 61801 and E. E. Hartwig, USDA, Stoneville, MS 38776. The collection is divided into 4 categories: Plant Introductions, T lines (genetic mutants), named cultivars, and G. gracilis. Glycine gracilis Skvortz. has been described as a species morphologically intermediate between G. max and G. soja Sieb. and Zucc. (Skvortzow, 1927), but Hermann (1962) placed it under synonymy with G. max. For this study G. gracilis has been separated from G. max.

The results of the screening data are presented in Table 1. Of the 2137 soybean plant introductions (PI) screened, the following 13 lacked SBL: PI 81,764, PI 82,278, PI 89,772, PI 89,773, PI 90,490, PI 90,763, PI 90,768, PI 96,786, PI 123,587, PI 157,492, PI 171,428, PI 171,431 and PI 291,310C. Of the 107 lines tested in the type collection,

Table 1
Distribution of alleles of the Le locus in the USDA
soybean germplasm collection

Collection	<u>Le</u>	<u>le</u>	Total
Plant Introductions			
Japan	500	0	500
China	811	10	821
Korea	436	3	439
India	245	0	245
USSR	16	0	16
Vietnam	5	0	5
Pakistan	4	0	4
Burma	2	0	2
Afghanistan	4	0	4
Indonesia	33	0	33
Malaya	14	0	14
Philippines	20	0	20
Thailand	34	0	34
Type collection	106	1	107
Named cultivars			
Southern	110	0	110
Northern	266	4	270
<u>Glycine gracilis</u>	40	0	40

only T102 was found to be lacking SBL. T102 is the source for y_4 , a chlorophyll-deficient gene. It was selected out of Wilson-5, a cultivar lacking SBL. All 110 of the named cultivars in the southern collection had SBL. Of the 270 named cultivars tested from the northern collection, only 4, which were previously reported by Pull et al. (1978b), lacked lectin. All of the Glycine gracilis accessions contained lectin.

The absence of lectin in seed does not appear to be associated with flower color, pubescence color, pod color, seed coat luster, seed coat color or hilum color. Most of the accessions without lectin are in Maturity Groups III or IV. All of the accessions without lectin come from either China or Korea.

In summation, 2664 lines in the USDA soybean collection were screened for the absence or presence of the 120,000 dalton seed lectin. A total of 18 accessions were found to be lacking the lectin.

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3) Relay intercropping of soybeans and small grains.

During the past two years we have been comparing several cropping systems: relay intercropping of soybeans with wheat, relay intercropping of soybeans with oats, and soybean monoculture. The purpose of the study was to determine if a need for separate breeding programs for these specialized cultural practices exists. Last year McBroom et al. (1979) reported a significant cultivar x cropping system interaction that would seem to indicate that such a need did exist. Further investigation of this cultivar x system interaction was carried out at two locations in Illinois, Urbana and DeKalb, during the summer of 1979.

At Urbana we planted 12 cultivars representing Maturity Groups I-IV in wheat, in oats, and also in monoculture. We used experimental designs that would allow comparisons of soybean yields in the intercropping and monoculture systems. The wheat and oats were planted in 41 cm rows to allow for interplanting of the soybeans. The planting dates of the soybeans were chosen to coincide with heading dates of the small grains. The soybeans in wheat and the associated monoculture were planted on May 29; the intercropped and monoculture soybeans with oats were planted on June 14. Those with oats, however, because of lack of moisture, did not start to germinate until June 22. The wheat was harvested July 2 and the oats were harvested July 19. The soybeans were harvested as they matured from October 6 through October 20.

Similar experiments were conducted at DeKalb, using seven of the same cultivars, those in Maturity Groups I-III. The soybeans were planted in wheat and monoculture June 12, and in oats and monoculture June 25. The wheat was harvested July 17 and the oats were harvested August 2. The soybeans at DeKalb were harvested November 11 and 12. At both Urbana and DeKalb in 1979 two rows 41 cm apart and 4.88 meters long were harvested for yield data. Notes were also taken on lodging, plant height, and number of branches per plant just prior to harvest. An analysis of variance of soybean yields was made for each experiment separately and then on the combined data over years and locations. Since we would like to make inferences over years and locations the data presented here will be the combined data. One way of looking at the combined data is to calculate a mean value for each cultivar intercropped and a mean value for each cultivar in monoculture over years and locations. An analysis of variance can be performed on these mean values using a pooled estimate of error from the various experiments to perform F-tests.

When such an analysis is done the intercrop and monoculture systems are significantly different, and the cultivars are significantly different, but the cultivar x system interaction is non-significant. Another way to analyze the data is to include sources of variation due to years and locations and various interactions with these terms. In such an analysis there are significant year x cultivar and location x cultivar interactions of sufficient magnitude that cultivars, when tested against these, are not considered significantly different. These two interactions cause complications in evaluation of the cultivar x system interaction and seem to be of a much greater magnitude, i.e., differences between years and locations seem to have a greater effect on cultivar evaluation than differences between cropping systems.

Table 1 contains the mean values for the seven cultivars grown over both years and at both locations. These are the means over all intercrop and monoculture plots grown. The pooled estimate of experimental error was used to calculate a lsd value and those yields not followed by the same letter are considered significantly different. It is noteworthy that the correlation ($r = .8877$) between these mean yields (intercrop vs. monoculture) is highly significant. Seven values are really not enough for a good estimate of the correlation coefficient. But if we calculate the correlation between yield in intercrop and yield in monoculture within each experiment using means, we have a total of 51 pairs of means correlated. Such a correlation coefficient ($r = .6164$) is highly significant. Furthermore, an overall correlation ($r = .6161$) of rankings of means within each experiment was highly significant. It is interesting that, over all cultivars, years, and locations, the

Table 1
Mean yields of soybeans intercropped and grown in monoculture

Cultivar	Intercrop yield (kg/ha)	Monoculture yield (kg/ha)
Cumberland	1826 a	3253 c
Oakland	1833 a	3008 a
Hark	1864 a	3035 a b
Wells	1906 a b	3238 b c
Beeson	2104 b c	3436 c d
Corsoy	2174 c	3371 c
Harcor	2309 c	3602 d

intercropped soybean yields averaged 61% of monoculture yields. The range of this percentage for individual experiments was from 42 to 80%. 'Williams' soybeans intercropped in wheat at Urbana, 1979, gave the best overall productivity with 4955 kg/ha of wheat and 3552 kg/ha of soybeans being produced.

On the basis of these means the extra effort and money required for a separate breeding program for intercropping apparently is not justified. However, a word of caution should be added. We worked with a rather small sample of cultivars, whose parentages are not very diverse, and which were all selected for their performance in a monoculture system. It could well be that a more diverse group of germplasm would give different results.

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R. L. McBroom
H. H. Hadley
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4) Inheritance of hard seeds in soybeans.

During the past three years we have studied the inheritance of hard seeds in soybeans. These studies have been supported in part by INTSOY and in part by the Rockefeller Foundation. They were begun with the help of Dr. H. C. Minor and Dr. E. H. Paschal III who had evaluated potential parental material for the hard-seed characteristic and who continued to help through advice, handling plant materials in Puerto Rico, and providing certain facilities.

Parental materials were classified as high, medium, and low in respect to hard-seed percentage. 'Barchet' and PI 326,578 with 70% and 93% hard seeds, respectively, were considered to be high, PI 240,672 and PI 32,566 with 33% and 37% were considered medium, and 'Hardee' and SJ2, each with less than 1%, were considered low in hard-seed percentage.

Seeds were obtained from individual parental, F_1 , and F_2 plants grown in Puerto Rico. In March, 1979, hand-threshed seed were shipped to Urbana. All undamaged seed were placed in a germinator and hard-seed counts were made five days later.

Frequency distributions of hard-seed percentage classes shown in Table 1 are examples of the type of data obtained. Barchet x Hardee and Hardee x

Table 1

Frequency distributions and mean percentages of hard seeds in parental,
F₁, and F₂ generations of four soybean crosses

Generation	Class											No. of plants	Hard seed X (%)
	0	0.01-10	11-20	21-30	31-40	41-50	51-60	61-70	71-80	81-90	91-100		
Barchet (P ₁) x Hardee (P ₂)													
P ₁					1	8	9	4	3	2		27	68.2 ± 1.92
P ₂	26	2										28	0.1 ± 0.07
F ₁	6	1										7	1.0 ± 1.14
F ₂	53	18	2	0	4	2						79	4.4 ± 1.24
Hardee (P ₁) x PI 326,578 (P ₂)													
P ₁	30											30	0.0 ± 0.00
P ₂							4	7	12	4		27	81.5 ± 1.36
F ₁	16	4	2									22	1.3 ± 0.83
F ₂	53	28	2	2	5	4	1					75	6.3 ± 1.47
Hardee (P ₁) x PI 323,566 (P ₂)													
P ₁	27	3										30	0.2 ± 0.10
P ₂	9	11	3	1	1							25	4.9 ± 1.65
F ₁	3	4	4	3	1	1	2					18	18.3 ± 2.61
F ₂	32	10	12	9	8	7	2	4	3	0	1	88	19.5 ± 2.62
PI 326,578 (P ₁) x Barchet (P ₂)													
P ₁						1	6	4	7	8		26	81.4 ± 1.24
P ₂						3	4	5	7	1		22	73.3 ± 1.40
F ₁					1	1	1	2	3	2		10	77.0 ± 3.88
F ₂						5	7	18	28	14		72	79.0 ± 1.04

PI 326,578 represent high x low (or low x high) crosses. Normal (soft) seed appears to be dominant. No evidence of transgressive segregation is obvious. Chi-square tests for goodness of fit on the basis of an assumed difference between the parents of three major genes, with complete dominance at each locus and only the completely recessive genotype being as high as the high parent, gave small values with probabilities of 20-50%. A similar hypothesis, except with an assumption of a difference of four major genes, was even more acceptable for the cross, Hardee x PI 326,578, but unacceptable for the cross, Barchet x Hardee.

The cross, Hardee x PI 323,566 (low and medium) showed evidence of "hybrid vigor" for hard-seed percentage with the mean values of F_1 and F_2 being almost four times as high as that of the high parent (18.3% or 19.5% vs. 4.9%). Another medium x low cross involving different lines, however, did not show heterotic-like behavior.

The high x high cross (PI 326,578 x Barchet) showed overlapping among samples of the four generations tested for hard-seed percentage. Both F_1 and F_2 means (77.0% and 79.0%) fell between those of the parents (73.3% and 81.4%). A quantitative genetic model (Mather and Jinks, 1971) was used to estimate gene effects. Only additive effects were significant. We have assumed that these high hard-seed parents differ only in minor or modifier genes.

Results of our studies appear to be similar to those reported by other soybean workers including Woodworth (1933), Kilen and Hartwig (1978), and Green and Pinnell (1968).

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1) Linkage tests between the A_p and W_1 loci.

The F_2 generation of the cross 'Williams' x 'Manchu (Madison)' was used to determine if the A_p and W_1 loci were linked. The A_p locus controls a seed acid phosphatase which exists in the germplasm in three different electrophoretic forms controlled by three codominant alleles-- A_p^a , A_p^b , and A_p^c (Hildebrand *et al.*, 1980). The W_1 locus controls flower color--purple (W_1) and white (w_1).

The W_1 genotype of F_2 individuals was determined by observing hypocotyl color of germinating seeds. Plants with purple hypocotyls have purple flowers. The A_p genotype was determined by electrophoresis (Hildebrand *et al.*, 1980).

The results of the linkage study are presented in Table 1. In the table $a = A_p^b A_p^b W_1$, $b = A_p^b A_p^c W_1$, $c = A_p^c A_p^c W_1$, $d = A_p^b A_p^b w_1 w_1$, $e = A_p^b A_p^c w_1 w_1$, and $f = A_p^c A_p^c w_1 w_1$. The chi-square test for independent assortment was used to determine whether linkage was present. The chi-square test for independence was 1.64 with 2 degrees of freedom, indicating that the A_p locus is inherited independently of the W_1 locus.

Table 1
 F_2 linkage test of A_p and W_1 loci, from the cross Williams
($A_p^b A_p^b w_1 w_1$) x Manchu (Madison) ($A_p^c A_p^c W_1 W_1$)

a	b	c	d	e	f	Sum	% R
21	44	28	11	22	8	134	I

Reference

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1) Heritability and correlation estimates for protein, oil, and crushing hardness in photo-sensitive and insensitive groups of soybean.

Protein, oil, and crushing hardness as an indicator of cooking quality are the important seed attributes for which soybean is valued in all parts of the world. Protein and oil content have been reported to be influenced by genetic and climatic factors (Chapman *et al.*, 1976; Shorter *et al.*, 1977) but with respect to crushing hardness attribute of soybean seed, information available in the literature is as good as nil. In the present communication, attempts have been made to understand the nature of genetic effect through heritability and other genetic parameters of variability for both photo-sensitive and insensitive groups of soybean. Association of these attributes has also been studied.

Material and methods: Twenty-five photo-sensitive strains and 20 photo-insensitive strains were evaluated in two separate replicated trials at Haryana Agricultural University, Hissar, India during rainy season, 1974 and spring season, 1975, respectively. Protein content and oil content were determined on replication basis, after drying the samples in a hot air oven 60°C and storing in air-tight containers, according to the method of McKenzie and Wallace (1954) and Kartha and Sethi (1957), respectively. The crushing hardness (kg/seed) was judged in whole seed with the help of a hardness tester (Ogwa Seiki, Ltd., Tokyo, Japan).

Genotypic coefficient of variation, heritability estimates (broad sense), genetic advance, and genotypic and phenotypic correlation were estimated using the formulae suggested by Burton (1952), Hanson *et al.* (1956), Johnson *et al.* (1955) and Miller *et al.* (1958).

Results and discussion: The estimates of mean, range, phenotypic, genotypic and environmental variance and their coefficient of variation along with heritability and expected genetic advance expressed at 5% selection intensity for protein and oil content and crushing hardness for both photo-sensitive (set I) and insensitive (set II) groups are given in Table 1.

Analysis of variance indicated significant genotypic differences for protein content and oil content in photo-sensitive group and significant genotypic differences for oil content and crushing hardness in photo-insensitive

Table 1

Estimates of mean, range, components of variance, heritability,
and genetic advance for protein content,
oil content, and crushing hardness

Estimate of	Percentage protein content		Percentage oil content		Crushing hardness	
	Set I	Set II	Set I	Set II	Set I	Set II
Mean	41.99	38.23	16.12	18.32	16.23	15.78
Range	36.10- 49.58	37.87- 41.48	13.82- 19.07	12.82- 23.59	14.03- 19.10	11.12- 19.37
Phenotypic variance	15.09	---	4.31	17.05	---	6.62
Genotypic variance	8.98	---	1.15	7.96	---	1.075
Environmental variance	6.11	---	3.16	9.09	---	5.55
Phenotypic coefficient of variation (%)	9	---	12.80	22.53	---	16.31
Genotypic coefficient of variation (%)	7	---	6.60	15.39	---	6.57
Environmental coeffi- cient of variation (%)	5	---	10.90	16.40	---	14.90
Heritability (%) (broad sense)	59	---	26.68	46.67	---	16.23
Genetic advance	4.69	---	1.09	3.97	---	0.86
Genetic advance as percent of mean	11	---	6.76	21.65	---	5.45
S.E.(d) at 5% \pm	2.018	NS ^a	1.44	2.13	dNS ^b	1.665

^aNot significant.

^bDifference not significant.

group. The mean and range were comparatively high in photo-sensitive group for oil content in spite of smaller population. This might be due to the comparatively more favorable high temperature during pod filling period in spring crop as compared to rainy season crop which was sown as late as in August. However, the reverse was the situation observed for protein content,

for which both mean and range were high in photo-sensitive group. Highest protein in photo-sensitive group was recorded for PK-71-5 (49.6%) followed by UPSM-236 (49.5%), PK-73-119 (47.5%) which were statistically at par with PK-71-5. Highest oil content in photo-insensitive group was recorded for 'Harosoy' deciduous (23.6%) followed by 'Hark' (23.3%), 'Traverse' (23.3%) and PS-73-7 (21.4%) whereas in photo-sensitive group, PK-73-97 gave the highest oil content (19.7%) followed by PK-73-BP-1-8 (18.6%), JM-670 (17.8%), JN-703 (17.8%) and PK-73-51 (17.8%) which were all statistically at par with PK-73-97. The highest crushing hardness, for which genotypic differences were observed only in photo-insensitive group, was exhibited by UPSM-375 (19.37 kg/seed) followed by 'Goldsoy' (17.40 kg/seed). Interestingly, strains exhibiting high crushing hardness also had high protein, indicating some association between these two seed attributes.

In order to understand the exact nature of association, correlations were estimated at both phenotypic and genotypic level. Results revealed that protein content and oil content in the photo-sensitive group had inherent negative association as indicated by significant phenotypic (0.55%) and high genotypic correlation values. In the photo-insensitive group, there was an absence of genotypic differences for oil and protein content in this group. However, looking at mean value of both the traits, it was clear that the strain UPSM-366, which had highest protein content, exhibited the lowest oil content (12.8%). Similar was the situation in the photo-sensitive group where PK-71-5 showed the highest protein content but had the lowest oil content (13.9%). This confirms the stable negative association between oil and protein content as recorded in earlier studies (Kamel et al., 1970; Lal et al., 1973; and Shorter et al., 1977). If this association is due to tight linkage between high protein and low oil content, it might be possible to have recombinant having high oil and protein content by adopting appropriate breeding technique like inter-mating among segregants in F_2 generation of a cross between high oil and high protein parents.

As there were no significant differences for protein content in photo-insensitive group and for crushing hardness in photo-sensitive group, the correlation of crushing hardness was only estimated with oil content and not with protein content in either of the groups. However, mean value indicated some positive association between protein content and crushing hardness as discussed earlier where protein lines were also having high crushing hardness. At present, information regarding the association of protein content and

crushing hardness of seed in literature is nil. Similarly there is no report regarding the association of hardness of seed with oil content. In the present material, crushing hardness had non-significant negative phenotypic correlation value (0.07) indicating absence of any association between these two attributes of soybean seed.

These correlations suggest that in order to incorporate good cooking quality (less crushing hardness), one has to sacrifice high protein content. However, it would be possible to incorporate both high oil content and good cooking quality.

Genetic gains in a population for the attributes under consideration would depend upon the genetic parameters of variability (Table 1) along with selection pressure. For protein content, on partitioning the observed variability which was significant only in photo-sensitive group, it was found that genotypic variance was higher than environmental variance, indicating more influence of genetic effects for the expression of protein content. However, in the photo-insensitive group, though the range was high, the absence of genotypic differences indicated the higher influence of environmental effects for protein content. With respect to oil content, variance and coefficient of variation at genotypic level were higher in photo-sensitive group as compared with insensitive. However, in both groups, genotypic variances were less than environmental variances, suggesting larger influence of environmental effects on oil content though appreciable genetic effects were also noticed. The influence of environmental effects was more in the case of photo-sensitive group. For crushing hardness, most of the observed variation in the photo-sensitive group was due to environmental effects whereas in the photo-insensitive group, though there was large influence of environmental effects, yet there was an appreciable influence of genetic effects.

For protein content, with the estimated heritability value (59%) in the photo-sensitive group, the expected genetic gain expressed as percent of mean, at 5% selection intensity would be 11%. For crushing hardness, in the photo-insensitive group having heritability estimate of 16.23%, the expected gain expressed as percent of mean would be only 5.45%. For percent oil content, high heritability (46.67%) was associated with high genetic gain expressed as percent of mean (21.65%) in the photo-sensitive group. In general, protein content had high heritability in the photo-sensitive group and oil content had high heritability only in the insensitive group. Shorter et al. (1977) also

reported high heritability for oil and protein content in soybean. Crushing-hardness showed comparatively poor heritability.

Summary: Thirty-five strains of photo-sensitive and 20 strains of photo-insensitive groups were evaluated for oil, protein and crushing hardness of seed in soybean at Hissar, India during spring and the rainy season, for genetic parameters and correlation. Oil content had inherent negative association with crushing hardness, an index of cooking quality. Heritability for oil content in the photo-sensitive group was average, whereas it was low for crushing hardness. Genetic gain at 5% selection intensity would be 11% and 21.65% and 5.45% for protein content, and hardness respectively. Environmental influence was larger as compared with genetic effects for oil and crushing hardness whereas for protein content, genetic effects were larger. Correlation study indicated that less crushing hardness could be combined with high oil and protein content.

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1) Genetic and altitude effects on seed protein content in soybean.

Summary: Sixty germplasm lines were raised in replicated trial at 700 m above m.s.l. and 1300 m above m.s.l. in the western zone of sub-Himalayan region to understand the genetic and altitude effects on seed protein in soybean. A larger influence of genetic effect was recorded; however, an appreciable influence of altitude, and genotype x altitude interaction effects were also noticed. Expression of protein content was maximum at the lower altitude, as compared with higher altitude. At lower altitude, the range was from 38.28 to 47.25% whereas at higher altitude, it was from 30.40 to 43.31%. EC14451 genotype exhibited high and stable protein content over altitude (43.32%). Various other genotypes also had above-average protein content. On the basis of high heritability (62.7%) recorded in the present study, the expected genetic gain expressed as percent of mean, would be around 14% at 5% selection intensity.

Introduction: Seed protein content in soybeans and other grain legumes depend on its genotypic constitution and environmental factors (Kamal et al., 1970; Gupta et al., 1974). Due to considerable influence of locations and seasons, genotypic difference among genotypes should not be based on the estimates of one season and one location. Introduction of soybeans is being attempted vigorously in India as a good oilseed and pulse crop. Hilly areas in the country were the first to have taken up its cultivation. Present study was undertaken to assess the genetic variation for protein content in the exotic collections and influence of altitudes and growing season on this character.

Materials and methods: Fifty exotic germplasm lines and ten extensively evaluated varieties of soybean were sown in randomized block design with two replications at Kulu, situated at an altitude of 1300 m on July 12, 1973, with a plot size of 2.7 m^2 and at Kangra situated at an altitude of 700 m on June 18, 1973, with a plot size of 2 m^2 . A dose of 20 kg N plus 80 kg P_2O_5 per hectare was applied at the time of sowing to the experimental plots. Crude protein was determined on replication basis according to A.O.A.C. (1960) specification. Appropriate statistical analysis was carried out as per Panse and Sukhatame (1961). Heritability and expected genetic advance were estimated by the formula suggested by Warner (1952) and Johnson *et al.* (1955).

Results and discussion: Breeders have long been aware of the problem of genotype-environmental interaction which contributes substantially to the non-realization of expected genetic gains from selection for the economic trait under consideration whether it is seed yield or protein content (Comstock and Moll, 1963), but the main difficulty has been in measuring this component of variability. One approach to such measurement which has been used in the present study is to grow a set of genotypes under diversified environments and from a combined analysis of variance of such experiments, extract measures of genotype x environment interaction (Sandison and Bartlett, 1958).

The results obtained in the present study from individual and combined analyses of variance for 60 genotypes evaluated at the different altitudes are given in Table 1. Analysis of variance indicated highly significant differences among the various genotypes studied at both the altitudes (Kulu and Kangra) suggesting the presence of sufficient genetic variation for the protein content. The combined analysis of variance, where total observed variability for the expression of protein content is partitioned into genotypic, altitude, and genotype x altitude interaction components after removing the experimental error component, revealed that mean sum of square (m.s.s.) due to all these three components was highly significant from experimental error component. The m.s.s. due to genotypes was also highly significant from the significantly genotype x altitude interaction m.s.s. This indicated the role of genetic, altitude, and genotype x altitude interaction effects for the expression of protein content in soybean. The magnitude of variances due to genotype (σ^2_g), genotype x altitude interaction (σ^2_{gl}), altitudes (σ^2_l), and experimental error or variation due to unknown factors (σ^2_e) as estimated from the expected m.s.s. as per Panse and Sukhatame (1961), were 12.765, 4.53,

Table 1
Analysis of variances for protein content in soybean

Altitude	Source due to	d.f.	M.s.s.
Kangra 700 m above m.s.l.	Genotypes	59	6.33*
	Error	59	2.25
Kulu 1300 m above m.s.l.	Genotypes	59	18.84*
	Error	59	3.87
Combined over altitudes	Genotypes	59	63.18*
	Altitudes	1	851.84*
	Genotypes x altitude	59	12.12*
	Pooled error	118	3.06

6.997, and 3.06, respectively, and the relative contribution of these components would be 46.67%, 16.56%, 25.58%, and 11.19%, respectively, for the protein content expression. This indicated the larger influence of genetic effects for grain protein in soybean. However, there was an appreciable influence of altitude. Similar results have also been reported by Gupta *et al.* (1974) in chickpea and Meiyani *et al.* (1977) in wheat.

In soybean, most of the earlier reports have revealed the larger influence of environments and agro-climatic factors on protein content (Cartter and Hartwig, 1963; Kamel *et al.*, 1970; Kesasvan and Morachan, 1974; Chapman *et al.*, 1976). However, these and some other workers have also reported varietal differences for protein content but they have ignored the effect of experimental error and altitude (Lal *et al.*, 1971; Sood *et al.*, 1977). To quantify whether high expression of protein content is at lower or higher altitude, environmental index (Finlay and Wilkinson, 1963) expressed as deviation of each altitude mean over genotypes from the grand mean over altitudes and genotypes ($39.1\% \pm 0.22$), was estimated for Kulu (-2.7) and Kangra (2.7). This estimate indicated the significant superiority of lower altitude over high altitude for the maximum expression of protein content in soybean.

At lower altitude (Kangra), this might be due to availability of larger green leaf area and high photosynthetic activity due to high rainfall and comparatively high average minimum temperature during vegetative growth and seed developmental phases (Table 2).

Table 2
Average (over past 5-10 years) monthly meteorological observations
during growing period of soybeans at lower (700 m above m.s.l.)
and higher (1300 m above m.s.l.) altitudes

Meteorological observations	Altitude	Months					
		June	July	Aug.	Sept.	Oct.	Nov.
Average mean temp. (C°)	Low	26.5	25.5	25.0	24.3	21.3	15.4
	High	24.3	23.8	24.0	22.0	19.5	15.4
Average minimum temp. (C°)	Low	17.5	21.3	21.0	18.8	14.2	8.4
	High	18.5	17.7	18.5	15.1	10.6	5.1
Average maximum temp. (C°)	Low	35.5	29.7	29.0	29.7	28.4	23.0
	High	30.1	29.9	29.5	28.9	28.4	25.7
Average rainfall (mm)	Low	136.3	402.3	649.9	141.1	33.5	7.8
	High	25.3	60.1	58.2	19.7	10.4	1.9

From breeding angle, it would be desirable to examine the mean protein content of individual genotypes, at each altitude (Table 3). At Kangra, highest percentage protein content was obtained for IC 13056 (47.25%) which was also highest when averaged over altitude along with EC 14451 (43.31%). At Kangra, other genotypes which had protein content statistically at par with IC 13056 were 'Kandaghat', IC 547, EC 93595, EC 14451, IC 10684, IC 2716 and EC 14424 in order. Genotype EC 93596 gave the lowest protein value (38.28%) at Kangra. At Kulu, highest protein (43.31%) was obtained for the genotype EC 41318 and the lowest (30.40%) was for IC 7217. Other genotypes which had protein content statistically at par with EC 41318 (43.31%) at Kulu, were

Table 3

Sr. No.	Genotype	Kangra	Kulu	Sr. No.	Genotype	Kangra	Kulu
1	IC 326-1	46.37	38.50	31	EC 18226	43.13	34.56
2	IC 547	44.18	37.18	32	EC 18555	41.12	34.56
3	IC 574	41.12	31.93	33	EC 39494	40.90	37.18
4	IC 1619	43.53	37.19	34	EC 41318	43.09	35.43
5	IC 2043	43.09	35.82	35	EC 39483	43.97	37.18
6	IC 2063	43.96	36.53	36	EC 39486	42.65	36.09
7	IC 2241	45.28	36.84	37	EC 50086	40.47	35.65
8	IC 2716	43.53	38.46	38	EC 63298	42.66	39.37
9	IC 7217	42.22	43.31	39	EC 76753	38.93	36.93
10	IC 9452	38.93	33.25	40	EC 76756	42.87	39.81
11	IC 9454	42.87	34.12	41	EC 76758	42.22	37.62
12	IC 9460A	43.74	31.93	42	EC 93595	43.09	39.81
13	IC 10678	40.24	32.81	43	EC 93596	39.59	39.59
14	IC 10684	42.87	34.12	44	EC 93599	40.47	34.78
15	IC 13008	42.00	32.81	45	EC 93604	39.15	36.53
16	IC 13009	43.74	35.00	46	EC 93741	40.02	40.25
17	IC 13050	42.66	39.81	47	EC 93745	43.31	30.40
18	IC 13056	47.25	39.37	48	EC 93747	42.66	34.12
19	EC 329-4	41.99	40.68	49	EC 93748	43.53	35.21
20	EC 9308	43.74	41.69	50	EC 93751	45.28	31.72
21	EC 9309	45.06	41.56	51	Hardee	43.74	34.78
22	EC 14424	43.96	38.06	52	Bienville	42.00	32.15
23	EC 14425	44.40	38.28	53	Bragg	41.78	35.21
24	EC 14427	43.53	39.59	54	Hampton	42.43	33.90
25	EC 14450	42.87	35.43	55	Punjab-I	40.69	35.00
26	EC 14451	44.62	37.62	56	Lee	40.89	35.00
27	EC 14452	42.00	41.34	57	Jackson	42.87	34.33
28	EC 14475	42.86	39.15	58	Davis	42.87	32.59
29	EC 18108	42.00	33.68	59	Pickett	38.28	39.15
30	EC 18196	42.43	34.56	60	Kandaghat	42.22	40.25
				S.E. (Mean) = \pm 1.12			
				1.39			

EC 76756, IC 13050, EC 14451, IC 13009, EC 32924, EC 76756, EC 63298, IC 326-1, EC 93599 and EC 9309 (39.81%) in order. After confounding the effect of altitudes, the highest protein content (43.31%) \pm 1.236 was obtained for IC 13056 and EC 14451 and other genotypes which were statistically at par with the highest ones, were EC 41318, Kandaghat, EC 13050, IC 547, EC 63298, EC 13009, IC 94601, IC 2716, EC 76753, IC 10684, 'Lee', 'Davis', EC 93747, IC 326-1, EC 9309 and EC 76756. If one compares the genotypes having high protein and falling in the first non-significant group at both altitudes, EC 14451 happens to be the only genotype having stable high protein content over altitudes. This indicated that in spite of appreciable effects of altitudes and genotype altitude on the seed protein content in soybean, high protein genotype yielded consistently higher and had more protein in favorable environment. This genotype appears to be interesting from breeding point of view.

Genetic gain in protein content through breeding would depend upon its heritability and selection intensity. In the present material, heritability estimated as percent of $\sigma^2_g / \sigma^2_g + \sigma^2_{ga} + \sigma^2_e$ after eliminating the altitude effect on genotypes, was found to be 62.7 indicating very high heritability for protein content due to preponderance of high additive gene effects. The expected genetic advance expressed as percent of mean on the basis of above heritability estimate with 5% selection intensity would be around 14%.

With the above discussion, one can conclude that there is large influence of genetic effect on seed protein content in soybean; however, there is appreciable influence of altitude, and altitude x genotype interaction effects. There appears to be sufficient scope for upgrading the protein content through selection due to its high heritability recorded in the present material.

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1) Segregation patterns of some simply inherited traits in Glycine max x G. soja crosses.

As part of a genetic study of the relationships within the genus Glycine subgenus Soja we wish to report some observations on the inheritance of traits in crosses of G. max x G. soja and G. max x semi-wild ("gracilis") lines. The data to be discussed are contained in Table 1; the discussion will proceed on a locus by locus basis.

Fr locus: Segregation of non-fluorescing root phenotypes was observed in two crosses: 'Hark' (Fr) x PI 153,292 (a non-fluorescent semi-wild line) and 'Minsoy' (fr) x PI 342,622B (a fluorescent G. soja). All F_1 plants had fluorescent roots; F_2 segregation ratios were not significantly different from 3:1, fluorescent: non-fluorescent phenotypes.

The G. soja germplasm collection includes about 20% non-fluorescent root phenotypes (n = 370 examined). All F_1 plants and F_2 progeny of a reciprocal cross Minsoy (fr) x PI 407,294 (a non-fluorescent G. soja) displayed non-fluorescent roots indicating that the non-fluorescent factors occurring in these two lines are functionally allelic.

Pb locus: Pubescence tip shape segregated 3:1, sharp: blunt in two crosses: Hark (blunt) x PI 153,292 (sharp) and PI 407,292 (sharp) x Hark. All F_1 plants bore sharp pubescence. These data agree with the findings of Ting (1946). Blunt pubescent tip is rare in G. soja (ca. 2%). A blunt phenotype found in G. soja (PI 342,434) proved to be functionally allelic with pb in 'Wells' in the F_1 and reciprocal backcrosses.

Ep locus: The segregation of high and low seedcoat peroxidase levels was observed in a cross of Minsoy (ep) x PI 342,622B (G. soja, high). F_1 plant bore seeds with high levels of peroxidase in the seedcoats; the F_2 generation segregated 3:1, high: low. Low seedcoat peroxidase levels occur in less than 1% of the accessions in the G. soja collection. Low peroxidase levels found in PI 342,434 proved to be functionally allelic with ep as found in Wells in F_1 and reciprocal backcrosses.

Table 1
Segregation patterns of some simply inherited traits in
Glycine max x G. soja crosses

Cross	Segregating alleles	F ₁ phenotype	F ₂ phenotypes	χ^2	n
Hark x PI 153,292 (<u>gracilis</u>)	<u>Fr/fr</u>	RF (+)	54 RF(+) 20 RF(-)	0.162	74
	<u>Pb/pb</u>	sharp	20 sharp 5 blunt	0.333	25
Minsoy x PI 342,622B (<u>soja</u>)	<u>Fr/fr</u>	RF (+)	36 RF(+) 12 RF(-)	1.000	48
	<u>Ep/ep</u>	high	27 high 9 low	0.000	36
Hark x PI 342,622B (<u>soja</u>)	<u>T₁/t₁</u>	tawny	20 tawny 6 grey	0.051	26
PI 407,292 x Hark (<u>soja</u>)	<u>Pb/pb</u>	sharp	16 sharp 5 blunt	0.016	21
	<u>T₁/t₁</u>	tawny	20 tawny 6 gray	0.051	26
	<u>Fg₁/fg₁</u>	1T (<u>Fg₁</u>)	9 <u>Fg₁</u> ^a 12 <u>fg₁</u>	11.57**	21
	<u>Fg₂/fg₂</u>	1T (<u>Fg₂</u>)	19 <u>Fg₂</u> ^a 2 <u>fg₂</u>	2.68	21
	<u>Fg₃/fg₃</u>	1T (<u>Fg₃</u>)	18 <u>Fg₃</u> ^a 3 <u>fg₃</u>	1.29	21

^aActual phenotypes: 6 = 1T, 3 = 2T, 3 = 4T, 7 = 4t, and 2 = 7t.

**p > 0.05.

T₁ locus: The inheritance of tawny and gray pubescence was observed in two G. max x G. soja crosses: Hark (t) x PI 342,622B (T) and PI 407,292 x Hark. F₁ plants of both crosses had tawny pubescence; segregation ratios of F₂ progeny were not significantly different from 3:1, tawny : gray. Gray pubescence does not occur in G. soja.

Fg₁, Fg₂ and Fg₃ loci: The inheritance of flavonol glycoside compounds was observed in one cross: PI 407,292 (G. soja, flavonol glycoside group 2T) x Hark (group 7t). F₁ plants were classified as group 1T; a small (n=21) sample of F₂ progeny segregated 6-1T : 3-2T : 3-4T : 7-4t : 2-7t. Chi-square tests indicate that the segregation of Fg₂ and Fg₃ were not significantly different from 3:1; however, the segregation pattern of Fg₁ tested significantly different from the expected 3:1 ratio. This might simply be attributed to the small sample. However, Buttery and Buzzell (1976) have demonstrated that individuals containing both Fg₁ and Fg₃ (i.e., groups 1T, 1t, 3T and 3t) have significantly lower photosynthetic rates than individuals of other genotypes. The plants examined in this study were grown in the field and no attempt was made to insure the survival and adequate sampling of possible subvital individuals. This significant Chi-square may be the result of inadequate sampling measures. Additional crosses of G. max x G. soja have been made and inheritance of traits will be established.

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1) The monogenic and digenic control of hypocotyl and flower color in soybeans.

The pigmentation of seedling hypocotyl is important in the knowledge, at a very early stage, of success in the cross of plants differing in this aspect.

Several genes, among which are W₁, W₂, W₃, W₄, and w_m, have been recognized as controlling flower pigmentation, and many studies indicate that flower and hypocotyl colors are closely associated. Hartwig and Hinson (1962) put in evidence that hypocotyl of W₁W₃W₄ genotypes is darker than that of W₁w₃W₄ ones. Bernard and Weiss (1973) reported that purple hypocotyl is controlled by the W₁ gene having a pleiotropic effect.

Aim of this report is to present some data showing monogenic and digenic segregation ratios for hypocotyl and flower pigmentation and to forward indications of pleiotropic effects of two complementary genes controlling flower color.

Crosses were made between plants of American and Japanese varieties judged interesting for their yield components (Olivieri *et al.*, 1979). F_1 plants were raised in summer 1978 and F_2 seed was sown on May 18, 1979 in plots distributed according to a randomized block design with three replications. Pigmentation was recorded assigning two classes of color.

Segregation ratios for hypocotyl and flower color are reported in Tables 1 and 2, respectively. Indications of monogenic control are evident for all cross combinations, with the exception of 'Mikawashima' x XK 505 whose segregation fit a 9:7 ratio. For this cross two complementary genes are involved in the control of hypocotyl and flower pigmentation and, if the same genes control both traits (as it is supposed by several studies), then both of them have a pleiotropic effect.

Table 1
Segregation for hypocotyl seedling color

Crosses	Observed number		Segregation 3:1		Segregation 9:7	
	Purple	Green	χ^2	P	χ^2	P
Mikawashima x Wells	101	30	0.308	0.75-0.50		
Mikawashima x SRF 150	198	66	0.000	0.99		
Mikawashima x XK 505	47	26	4.388	<u>0.05-0.02</u>	1.962	0.25-0.10
Mikawashima x Beeson	103	43	1.543	0.25-0.10		
Mikawashima x Caloria	107	26	2.108	0.25-0.10		
Mikawashima x Corsoy	87	36	1.548	0.25-0.10		
Traverse x Extra Early	78	29	0.252	0.75-0.50		

Table 2
Segregation for flower color

Crosses	Observed number		Segregation 3:1		Segregation 9:7	
	Purple	Green	χ^2	P	χ^2	P
Mikawashima x Wells	51	16	0.044	0.90-0.75		
Mikawashima x SRF 150	106	35	0.002	0.95-0.90		
Mikawashima x XK 505	20	15	5.952	0.02-0.01	0.011	0.95-0.90
Mikawashima x Beeson	57	17	0.162	0.75-0.50		
Mikawashima x Caloria	93	21	2.632	0.25-0.10		
Mikawashima x Corsoy	46	15	0.005	0.95-0.90		
Traverse x Extra Early	75	35	2.727	0.10-0.05		

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1) Changing the maturity of soybean cultivars using EMS.

This study was conducted to determine if the mutagenic agent, ethyl methane sulfonate (EMS), could be used to change the maturity of a soybean line while still maintaining the yielding ability and other morphological characters of the line. Mutants with changes in maturity have been reported

in several experiments (Kawai, 1970); however, there are few reports where soybeans have been used in studies of this kind.

In the study 1000 seeds of the cultivar 'Williams' were allowed to imbibe water for 16 hours by being soaked in distilled water that was aerated. The seeds were then soaked in a .05M EMS solution (buffered with NaOH to pH 7.0) for 8 hours with continuous aeration (Constantin *et al.*, 1976). The seeds were then washed in distilled water and planted immediately. In addition, control seeds were planted that had been soaked in aerated distilled water for 24 hours.

The M_1 seeds were harvested in bulk and planted the next year along with untreated controls. In the fall single plant selections were made of the plants maturing later than the control. Over 100 plants were selected that appeared to be later than Williams. The seeds of each single plant selected were grown in individual rows the next year and the rows evaluated for maturity, yield and other characters. Those selections which had later maturity, equivalent yields, and were similar to Williams in other characteristics, were planted in four-row plots for further evaluation. A few of the selections had some sterile plants in the plots so they were not evaluated further. Thirty selections that were later maturing than Williams were grown in four-row plots at two locations with three replications per location. The comparison of Williams and 12 late maturing selections for yield, physiological maturity, 95% brown pods, and plant height is shown in Table 1. Notes were taken on other characters such as flower color, pubescence color, and hilum color and all plants in each selection were the same as Williams for these characters.

There were no significant differences in yield or plant height among the lines; however, lines which were significantly later in physiological maturity and 95% brown pods than Williams were found. Thus it appears that the maturity of a line can be changed, at least to a later maturity, while maintaining yield.

This technique may have application in breeding programs, particularly where one may want later maturing selections in lines with disease, insect or pest resistance. Finding mutations for lateness may be easier than finding mutants with earlier maturity, although both types have been found (Gustafsson and Lundqvist, 1976). When using this method it is advisable to grow the M_1 , M_2 , and M_3 generations in isolation and remove any sterile plants to reduce the possibility of outcrossing.

Table 1

Yield, physiological maturity, 95% brown pods, and plant height of late maturing selections from EMS-treated Williams seed

Selection	Yield (bu/acre)	Physiological maturity	95% brown pods	Plant height (in.)
Williams	47.3	26 Sept.	6 Oct.	39
301	46.5	2 Oct.	17 Oct.	36
405	50.3	7 Oct.	20 Oct.	40
603	46.3	6 Oct.	17 Oct.	37
707	45.5	5 Oct.	17 Oct.	38
709	48.0	3 Oct.	17 Oct.	40
713	47.0	3 Oct.	15 Oct.	39
913	45.4	3 Oct.	12 Oct.	37
1205	46.5	5 Oct.	18 Oct.	41
1214	49.2	6 Oct.	20 Oct.	41
1302	46.9	4 Oct.	18 Oct.	38
1309	47.6	2 Oct.	10 Oct.	36
1406	47.9	4 Oct.	15 Oct.	37

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1) Evaluation of soybean germplasm for resistance to corn earworm--IV.*

Corn earworm (Heliothis zea-Boddie) is one of the most destructive pests of soybeans (Glycine max [L.] Merrill). It feeds on foliage as well as developing pods. Each larva is capable of damaging 6 to 8.2 pods or 7.1 seeds between 4th to 6th instar (both inclusive) (Boldt et al., 1975; Smith and Bass, 1972). Some cultivars have been found to be resistant to foliage feeding by corn earworm (Beland and Hatchett, 1976; Clark et al., 1972; Joshi, 1977; Joshi and Wutoh, 1976; Hatchett et al., 1976) but to date no cultivar has been reported to resist pod damage from this pest. This study was undertaken to evaluate the extent of pod damage from corn earworm on certain soybean cultivars.

Materials and methods: Twenty-one soybean cultivars belonging to Maturity Group IV were evaluated for pod damage resistance during 1974 and 1975 in the screen house at the University of Maryland, Eastern Shore, Princess Anne. Ten seeds of each cultivar were sown on May 14 in both years, the seeds being 5 cm apart within the row and rows being 91 cm apart. Each cultivar was replicated 3 times. During 1974, 271 corn earworm moths were released in the screen house but in 1975, 416 moths were released in the same area. At maturity a random sample of 5 plants was taken from each cultivar. The number of damaged and undamaged pods/plant was recorded for each cultivar. Duncan's Multiple Range Test was used to test significant difference between the means.

Results and discussion: The mean numbers of undamaged and damaged pods/plant for each cultivar are given in Table 1.

During 1974, 'Oksoy' produced the highest number of undamaged pods/plant (45.4), followed closely by 'Custer' (44.4) and 'Columbus' (42.1). 'Funk Delicious', 'Boone', 'Carlin', 'Polysoy' and 'Cutler' produced significantly fewer pods/plant as compared with the rest of the cultivars. In 1975, Oksoy again produced the highest number of undamaged pods/plant (83.4) and the distant second was Columbus (43.7). Custer did not perform well in 1975. This may be due to increased insect pressure on the host plants during 1975.

*This is part of a SEA/USDA funded project.

Table 1
Mean number of undamaged and damaged pods/plant for
certain soybean cultivars

Cultivar	Undamaged pods		Damaged pods	
	1974	1975	1974	1975
Funk Delicious	6.5a*	9.0ab	0.7ab	0.1a
Boone	6.7a	5.0ab	0.2ab	0.5a
Carlin	7.8ab	21.2a-c	0.5ab	0.7a
Polysoy	12.2a-c	9.4ab	0.03a	1.3a
Cutler	15.1a-d	0.5ab	2.4b-d	2.6a
Midwest	18.9a-e	16.7a-c	2.5b-d	0.2a
Jefferson	20.8a-e	15.4a-c	1.8a-d	0.5a
AK (FC 30.761)	22.7a-e	13.8a-c	0.2ab	3.9a
Hurrelbrink	23.2a-e	17.9a-c	0.5ab	1.2a
Patterson	24.9a-e	22.9a-c	1.3a-c	3.0a
H.P. 963	27.7a-e	13.7a-c	1.0a-c	1.2a
Delmar	28.0a-e	17.7a-c	4.6e	0.5a
Wye	30.6a-e	26.5b-d	1.4a-c	3.1a
Emperor	32.7a-e	14.1a-c	3.0c-e	1.5a
Hong Kong	32.8a-e	4.1a	1.5a-d	0.6a
Kent	35.3b-e	17.9a-c	3.7de	1.1a
D67-3297	36.1c-e	33.1cd	1.1a-c	1.5a
AK (Kansas)	38.4c-e	20.1a-c	1.2a-c	0.6a
Columbus	42.1de	43.7d	1.2a-c	2.8a
Custer	44.4e	15.4a-c	2.0a-d	0.5a
Oksoy	45.4e	83.4e	1.7a-d	1.5a

* Means not followed by the same letter differ statistically at the 0.05 probability level according to Duncan's Multiple Range Test.

The number of corn earworm moths released during 1975 was 1-1/2 times more than in 1974 for the same area. Out of 21 cultivars, the productivity of 17 cultivars (Table 1) decreased due to increased pest pressure but the productivity of 4 cultivars (Funk Delicious, Carlin, Columbus and Oksoy) increased

in 1975 as compared with 1974. Based on two-year average, Oksoy produced the highest number of pods/plant (64.4), followed by Columbus (42.9) and D67-3297 (34.6). These data indicated that Oksoy exhibited a high level of tolerance to corn earworm.

More damaged pods on a cultivar is a clear indication of host preference by the corn earworm. Then it follows that percent pod damage can be used as an index to express preference or non-preference by this pest. On the basis of two-year average, it appears that Oksoy (3% damaged pods) and AK (Kansas) were least preferred by corn earworm, followed closely by Custer and D67-3297 (3.5% damaged pods/plant). The data indicate that Cutler was highly preferred by corn earworm for pod damage in the screen house. Research workers engaged in host plant resistance research may want to examine some of these entries more critically for developing resistant soybean cultivars.

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2) Performance of soybeans, lima beans, and corn in pure and mixed culture.*

One of the main objectives of the National Aeronautics and Space Administration (NASA) is to develop a controlled ecological life support system (CELSS). Such a system is needed to harness solar energy for inhabitants of

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the earth and to set up manufacturing facilities in space. Before this gigantic step, NASA is interested in evaluating ground-based manned demonstration of CELSS (Mason and Carden, 1979). Higher plants will form one of the important components of CELSS. These plants will not only provide food and feed but also will play an important part in revitalizing air by removing CO₂ and adding O₂.

It has been reported that roots of certain plants exude certain chemical compounds which may depress the yielding ability of other crops when grown in close proximity. On the other hand, leguminous plants are known to exert beneficial effects on other crops growing close by.

Previous studies conducted for NASA clearly indicate the usefulness of soybean plant (Glycine max [L.] Merrill) in the development of CELSS (Phillips, 1977; Phillips et al., 1978). It has been suggested that 43% of the cropped area in the manufacturing facility in space be planted under soybeans (Phillips, 1977).

The objective of this study was to test compatibility of growing soybeans in mixed culture with corn (Zea mays) and lima beans (Phaseolus lunatus).

Materials and methods: Soybean cultivar 'Shore' was tested for its compatibility with corn ('6693 Pioneer') and lima beans (cultivar 'Henderson') in mixed culture in the field during 1978. The following treatments were evaluated:

- 1) soybeans in pure stand.
- 2) lima beans in pure stand.
- 3) corn in pure stand.
- 4) soybeans and corn in mixed culture (alternate rows).
- 5) soybeans and lima beans in mixed culture (alternate rows).

The experiment was laid out in a completely randomized block design with three replications. All treatments were planted on June 20, 1978. Each treatment consisted of four rows, rows being 6.1 m long and 0.9 m apart. Two center rows were treated as experimental rows. Sixty-one centimeter row length from each side in the experimental rows was treated as non-experimental, leaving 4.9 m as net experimental row length. Within the rows, corn seed was planted 20 cm apart, lima beans 8 cm apart and soybeans 4 cm apart. At maturity, two center rows of each treatment were harvested and seed yield was recorded. Seed yield is reported on the basis of single rows for all treatments. Lima beans were harvested on September 25 and 26, 1978; corn and soybeans were harvested on November 9, 1978. Data were analyzed statistically by

employing Duncan's Multiple Range Test.

Results and discussion: Yields from soybeans, lima beans and corn in pure and mixed stand are given in Table 1. These crops gave much higher yields in mixed culture than in pure stand. Soybean yield in pure stand was 497 g, but in mixed stand with corn, yield increased to 740 g. Though this increase in yield is quite substantial, the difference between these two treatments was not statistically significant. Soybeans in mixed culture with corn (alternate rows) appeared to have gained more height as compared to pure stand. The beneficial effect on soybean yield in mixed culture with corn may be due to increased plant height. Another factor which could have stimulated soybean yield might be moderation of extreme temperatures exerted by shading during day time.

Table 1
Yield of soybeans, lima beans and corn
in pure and mixed stand

Treatment	Yield/4.9 m row (g)
<u>Soybean yield</u>	
Pure stand	497.0a [†]
Mixed cultures with corn (alternate rows)	740.2ab
Mixed cultures with lima beans	1,051.0b
<u>Lima bean yield</u>	
Pure stand	202.3a
Mixed cultures with soybeans	374.8b
<u>Corn yield</u>	
Pure stand	1,024.2a
Mixed cultures with soybeans	2,253.0b

[†]Means not followed by the same letter differ at the 0.05 probability level according to Duncan's Multiple Range Test (DMR). DMR Test was applied to each crop separately.

Soybean in mixed culture with lima beans gave highest yield (1051 g). Since both of these crops are leguminous, it appears that they exert a beneficial influence on each other. It may be noted that lima beans in pure stand gave considerably low yield (202 g). Similar results have been obtained with corn.

When different kinds of organisms benefit from a mutual association, the relationship between the organisms is called mutualism. These data clearly indicate mutualistic relationship between soybeans, lima beans, and corn. Mixed cropping seems to be a useful practice to follow for producing food and feed in the space colonies. This approach may also be useful in terrestrial agriculture from the standpoint of energy conservation in developed countries and limited availability of energy inputs in less developed countries.

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1) Isolation of soybean lectin specific polysomes by immunoadsorption.

Soybean lectin (SBL), a glycoprotein found in seeds, is capable of agglutinating red blood cells. SBL has a molecular weight of 120,000 daltons and is composed of four subunits of 30,000 daltons (Lis and Sharon, 1973). SBL protein comprises 0.5-5% of the total protein in defatted meal, depending upon the soybean variety used (Pull et al., 1978). The present report describes the isolation of SBL-specific polysomes from the cotyledons of maturing seed by

the use of an immunoadsorption procedure. This is the first step in a project to determine the molecular-genetic control and the processing events involved in lectin biosynthesis during seed maturation.

The immunological isolation of specific polysomes can be achieved if antibodies to purified protein interact with the nascent polypeptides attached to the polyribosome complex. In immunoprecipitation, a second antibody (anti-antibody) is used to precipitate the antibody-polyribosome complex (Shapiro *et al.*, 1974). More recently an immunoadsorption technique has been used to pull the antibody-polyribosome complex out of solution (Schutz *et al.*, 1977). In this method the second antibody was covalently attached to a cellulose matrix.

Soybean lectin was purified from either whole or defatted meal of variety 'Williams' (Maturity Group III) by affinity chromatography with N-acetyl-D-galactosamine (Allen and Neuberger, 1975). Rabbits were immunized with SBL subunits in 0.1% sodium dodecyl sulfate and 50% Freund's complete adjuvant. Anti-SBL antibodies were purified from immune sera by $(\text{NH}_4)_2\text{SO}_4$ fractionation and chromatography on an SBL-Sepharose column. Non-immune rabbit immunoglobulin was purified by $(\text{NH}_4)_2\text{SO}_4$ fractionation and DEAE-Sepharose chromatography. Serum from goats immunized against rabbit IgG was obtained commercially and the goat anti-rabbit antibodies were isolated by $(\text{NH}_4)_2\text{SO}_4$ fractionation and affinity chromatography on a rabbit IgG-Sepharose column.

Seeds were harvested during the maturation period and were divided into three weight ranges of 0.15-0.19, 0.20-0.24, and 0.25-0.29 g fresh weight per seed. Seeds were frozen at -70°C . Polysomes were extracted from 36 g of whole seed and were pelleted through a 50% sucrose cushion (Goldberg *et al.*, 1978). The polysome pellets were resuspended in approximately 15 ml of polysome buffer and were clarified by centrifugation for 5 min at $3000 \times g$. A total of 400-700 A_{260} units were obtained and were incubated with 2.0-2.5 μg of anti-SBL antibody per A_{260} unit. After incubation for 1.5 hr at 4°C the polysomes were applied at approximately 10 ml/hr to a 1×10 cm column containing 1 g of Sepharose covalently coupled to goat anti-rabbit antibody (GAR-Sepharose). All column procedures were performed at 4°C . After sample application, the column remained undisturbed for 2 to 18 hrs. The GAR-Sepharose was then washed sequentially at 50 ml/hr with the following buffers: 30 ml of 40 mM Tris, pH 7.5, 0.28 M KCl, 5 mM MgCl_2 , 50 $\mu\text{g/ml}$ heparin; 30 ml of 2% Triton - 0.5% Na deoxycholate in the same buffer; and 100 ml of buffer without

detergents. The bound polysomes were then dissociated by 20 mM EDTA (Schutz *et al.*, 1977) in 40 mM Tris-HCl, pH 7.5. The column effluent was measured for A_{260} . The GAR-Sepharose matrix was regenerated by an acid wash to remove bound antibody and could be used repeatedly.

In one set of experiments to demonstrate specificity of the polysome binding (Figure 1a), polysomes were applied to a GAR-Sepharose column without prior incubation with antibody. The unbound polysomes were collected and incubated with anti-SBL antibodies and reapplied to a second GAR-Sepharose column. Figure 1a shows that no A_{260} above the background absorbance of 20 mM EDTA was found in the effluent from the control column. In a second experiment (Figure 1b), polysomes were incubated with control IgG prepared from non-immunized rabbits and then applied to a GAR-Sepharose column. The unbound effluent from the column was reincubated with anti-SBL antibody and was reapplied to a second GAR-Sepharose column. Again, specific binding was not found in the control column but was found if polysomes had been incubated with anti-SBL antibody.

The results presented here strongly indicate that polysomes isolated from GAR-Sepharose are those active in synthesis of SBL polypeptides. Presently attempts are being made to isolate poly(A) RNA from the dissociated polysomes and to characterize it by electrophoresis in methylmercuric hydroxide gels (Bailey and Davidson, 1976) and by *in vitro* translation (Pelham and Jackson, 1976).

Williams soybeans at maturity contain approximately 2.5% of their protein as SBL. The GAR-Sepharose immunoabsorption technique was also used with polysomes extracted from maturing seeds of 'Sooty'. Sooty is one of several varieties which have been reported to lack any detectable SBL protein (Pull *et al.*, 1978). Sooty polysomes incubated with anti-SBL antibody did not bind to GAR-Sepharose (data not shown) indicating that polysomes active in SBL synthesis may not be present in Sooty. Confirmation of whether Sooty totally lacks SBL mRNA or lacks a functional SBL mRNA will require hybridization and other direct experiments.

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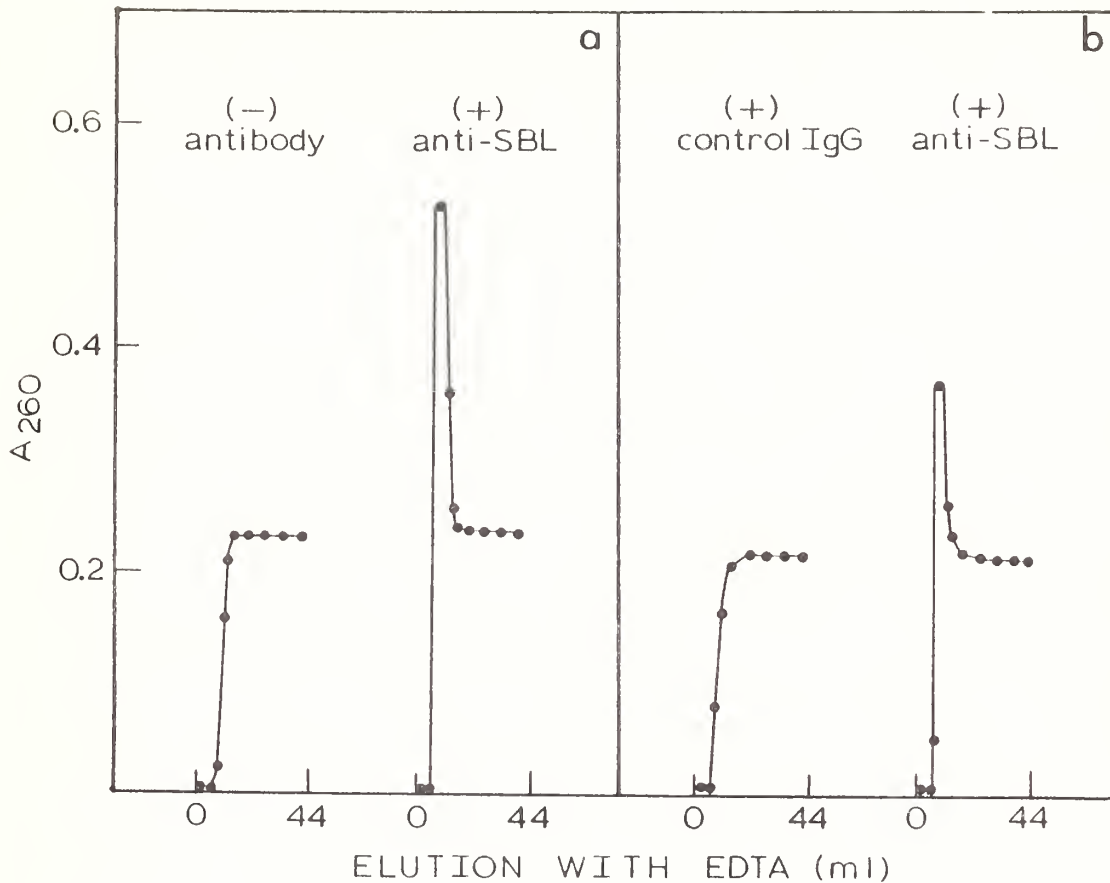


Figure 1. Dissociation of bound polysomes from GAR-Sepharose columns. In (a) seeds weighing 0.15-0.19 g were used and in (b) seeds of 0.25-0.29 g fresh wt per seed were used for polysome isolation. Polysomes were incubated with antibody as indicated and applied to GAR-Sepharose columns as described in the text.

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1) The effect of added methionine on the growth and protein composition of soybean on cotyledons.

Immature soybean cotyledons grow well in aseptic in vitro culture (Ann. Bot. 41: 29, 1977). The effect of adding methionine to a sulfur-adequate medium was tested. Methionine caused a dry weight increase of 23%. Methionine also raised the methionine content of the protein by 22% and decreased the arginine content by 11%. Preliminary data indicate that the latter changes are partially accounted for by an increase in the ratio of glycinin to conglycinin. The growth effect is apparently a result of the inability of the cotyledon to synthesize methionine fast enough because the transfer RNA for methionine had 18% more methionine attached to it when methionine was added.

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1) Evaluation of soybean germplasm collection for climatic conditions in Poland.

In 1974 studies were commenced to evaluate the variation in qualities and traits of soybean. The material covered a collection of 2412 entries including 275 varieties and 2137 genetic lines. The entries representing Maturity Groups (MGs) 00-IV were obtained from the following centers: U.S. Regional Soybean Lab., Urbana, Illinois, USA; Corn Breeding Lab., Hokkaido, Japan; National Agric. Exp. Sta., Hitsujigaoka, Sapporo, Japan; Weibullsholm Inst. Branch Sta., Fiskeby, Sweden; Dept. of Crop Science, Univ. of Guelph, Canada and Research Branch Canada Agric. Morden, Manitoba, Canada (41-58° northern latitude). They were all tested under field conditions in the vicinity of Poznan (51°30' northern latitude) in a full three-year cycle (1975-1977).

As expected, some of the entries failed to mature in particular years, others produced no seeds at all. Differences between the American classification of the MGs and our observations approximated 4-6 weeks. Evaluation of the collected forms was very rigorous. It resulted mainly from varying weather conditions characteristic of long rainless periods in late spring and early summer of 1975-1977. Another criterion for severe negative selection leading to removal of certain forms was the healthiness of plants. Approximately 40% of plants were removed due to viral and bacterial diseases.

After preliminary verification of rough results, 445 forms that matured in the field were taken for a synthetic evaluation including 11 morphological and developmental traits.

The range of variation within the analyzed traits was noteworthy (Table 1); e.g., the length of flowering period ranged from 7 to 63 days and that of growing period from 116 to 194 days. The plants were appreciably differentiated in height (21.0-152.0 cm) and in the height of the first pod formation as viewed from ground level (2.0-40.0 cm). Also, the seed yield parameters fluctuated (Table 1). Analysis of variance for the three years of study showed the values for certain traits to vary with years while the others to be less

Table 1

Variation of 11 soybean traits (1975-1977), Exp. Sta. Swadzim n. Poznan

Traits	Mean	Variance coefficient	Confidence interval	Range
1) Days to flowering	76.4	18.7	65.5- 66.7	56.0- 84.0
2) Flowering period, days	26.9	35.9	20.2- 21.7	7.0- 63.0
3) Maturity, days	169.6	12.4	140.7-143.3	116.0-194.0
4) Height, cm	72.9	30.9	46.1- 49.2	21.0-152.0
5) Branch, number	3.4	43.0	2.0- 3.2	1.0- 6.0
6) Height of 1st pod setting, cm	14.5	46.0	8.4- 8.9	2.0- 40.0
7) Pods, number per plant	24.4	43.9	24.3- 26.1	8.0- 54.0
8) Seeds, number per plant	40.1	48.3	38.6- 41.8	11.0-104.0
9) Seeds, number per pod	1.6	15.6	1.5- 1.6	1.1- 2.4
10) Yield per plant, g	6.2	58.2	7.4- 8.0	1.1- 21.2
11) Seed weight, g/100	15.4	35.0	19.5- 20.3	10.1- 36.0

dependent upon the climate, i.e., determined genetically to a large extent (Table 1). Worth emphasizing is the high stability of such a basic trait as growing period (the lowest variation coefficient 12.4%). The least stabilized trait was the seed/plant yield (variation coefficient 52.5%). Yet, the average seed/plant yield was 6.2 g which is considered satisfactory. Moreover, of the total population, 16.6% forms were selected whose seed/plant yield was above 9.1 g for the three experimental years. When growing 330,000 plants per hectare (at spacing 10 x 30 cm) the expected yield can be as shown in Table 2.

Early maturation was the major trait observed and on its background the variation of other traits was evaluated. Considering the mentioned discrepancies between the American classification of MGs and that in our climatic conditions, the 445 forms comprising population was conventionally divided into eight maturity groups (Table 3) and the groups tested for traits differing from each other significantly (Table 4).

The differentiation regarded primarily the date of bursting into flower, length of flowering period, and height of plants, besides the length of growing period. The groups I-IV (124-163 days of growing) were insignificantly

Table 2
Expected seed yield (kg/ha)

Yield per plant, g	Calculated seed yield, kg/ha	Number of items	Percent
≤ 3.03	1000	67	15.1
3.04- 4.54	1000-1500	71	16.0
4.55- 6.06	1500-2000	82	18.4
6.07- 7.57	2000-2500	85	19.1
7.58- 9.09	2500-3000	66	14.8
9.10-10.60	3000-3500	42	9.4
> 10.70	3500	<u>32</u>	<u>7.2</u>
		445	100.0

differentiated with respect to seed/plant yield. Between the remaining combinations of maturity groups statistically significant discrepancies were noted for a higher number of traits.

Another significant trait besides early maturation is the yielding capacity. On the basis of three-year observations, 50 forms were selected with a high and stable seed yield. The most promising are those characterized by a fair seed yield and satisfactory early maturity (growing period up to 140 days). Other forms represent very advantageous components for crossing.

A detailed analysis of the 445 forms revealed a number of interesting and significant correlations (Table 5). These make a very effective tool in the current selection work.

Observations made during flowering pointed to certain phenomena beyond the so-far gained knowledge of this species in Poland. Therefore careful examination of the process of flowering is continued.

The majority of analyzed soybean populations was characterized by determinate maturity (dt_1). In many instances pods formed on the top fruiting node semi-determined maturity. Leaf abscision at maturity followed the same pattern (Ab). Sporadically, single populations behaved differently.

Data for seed traits varied conspicuously, particularly those for the size. Seed weight, g/100 ranged from 10.0 to 40.0, sometimes from 50.0 to

Table 3
Maturity groups and characteristics of their traits

Maturity groups	Flowering period days	Number of items	Traits ^a										
			1	2	3	4	5	6	7	8	9	10	11
I	124-133	18	61.9	17.6	128.8	39.1	2.8	7.3	23.4	36.5	1.5	7.3	20.6
II	134-143	47	65.8	22.0	138.9	52.1	3.1	8.8	26.2	43.0	1.6	8.1	19.8
III	144-153	48	68.0	22.0	149.5	47.3	3.6	9.4	24.2	39.7	1.5	7.7	20.0
IV	154-163	33	66.6	28.0	158.6	65.3	3.2	9.8	27.9	48.0	1.7	8.3	18.3
V	164-173	36	68.3	32.0	170.0	76.2	3.0	10.8	30.8	54.7	1.8	9.2	17.6
VI	174-183	124	76.9	33.5	179.0	83.2	3.6	16.4	24.5	42.8	1.7	6.2	15.1
VII	184-193	129	88.3	33.5	186.0	84.5	3.5	19.9	20.1	32.5	1.6	3.5	11.1
VIII	194-	10	98.0	30.4	194.0	85.7	3.7	20.8	20.7	34.3	1.6	3.3	9.9

^aFor explanation, see Table 1, column 1.

Table 4
 Traits differing particular maturity groups
 (calculated upon multifactorial variance analysis)

Contrast	Maturity groups			Traits ^a
1	I	x	II	3, 4
2	I	x	II	1, 3, 4
3	I	x	IV	2, 3, 4, 8, 9
4	I	x	V	1, 2, 3, 4, 6, 7, 8, 9, 10
5	I	x	VI	1, 2, 3, 4, 6, 9, 11
6	I	x	VII	1, 2, 3, 4, 5, 6, 10, 11
7	I	x	VIII	1, 2, 3, 4, 6, 10, 11
8	II	x	III	3
9	II	x	IV	2, 3, 4
10	II	x	V	2, 3, 4, 6, 7, 8, 9, 10
11	II	x	VI	1, 2, 3, 4, 6, 10, 11
12	II	x	VII	1, 2, 3, 4, 5, 6, 7, 8, 10, 11
13	II	x	VIII	1, 2, 3, 4, 6, 10, 11
14	III	x	IV	2, 3, 4, 8, 9, 11
15	III	x	V	2, 3, 4, 7, 8, 9, 10, 11
16	III	x	VI	1, 2, 3, 4, 6, 9, 10, 11
17	III	x	VII	1, 2, 3, 4, 5, 6, 7, 8, 10, 11
18	III	x	VIII	1, 2, 3, 4, 6, 10, 11
19	IV	x	V	2, 3, 4
20	IV	x	VI	1, 2, 3, 4, 6, 10, 11
21	IV	x	VII	1, 2, 3, 4, 6, 7, 8, 9, 10, 11
22	IV	x	VIII	1, 3, 4, 6, 8, 10, 11
23	V	x	VI	1, 3, 4, 6, 7, 8, 9, 10, 11
24	V	x	VII	1, 3, 4, 6, 7, 8, 9, 10, 11
25	V	x	VIII	1, 3, 4, 6, 7, 8, 10, 11
26	VI	x	VII	1, 3, 6, 7, 8, 9, 10, 11
27	VI	x	VIII	1, 3, 6, 10, 11
28	VII	x	VIII	1, 3

^aFor explanation, see Table 1, column 1.

Table 5
Correlation coefficients

Traits ^a	1	2	3	4	5	6	7	8	9	10
1) Days to flowering										
2) Flowering period, days	-0.01									
3) Maturity, days	0.064xx	0.46xx								
4) Height, cm	0.28xx	0.44xx	0.57xx							
5) Branch, number	0.19xx	0.00	0.12xx	0.07x						
6) Height of 1st pod setting, cm	0.65xx	0.22xx	0.61xx	0.52xx	0.07x					
7) Pods, number per plant	-0.24xx	0.14	-0.16xx	0.07xx	0.29xx	-0.36xx				
8) Seeds, number per plant	-0.28xx	0.07xx	-0.15xx	0.12xx	0.23xx	-0.34xx	0.94xx			
9) Seeds, number per pod	-0.21xx	0.11xx	-0.04	0.16xx	-0.13xx	-0.09xx	0.19xx	0.42xx		
10) Yield per plant, g	-0.50xx	-0.12xx	-0.41xx	-0.09xx	0.02	-0.53xx	0.73xx	0.76xx	0.33xx	
11) Seed weight, g/100	-0.55xx	-0.33xx	-0.57xx	-0.38xx	-0.25xx	-0.53xx	0.05	0.05x	0.02	0.057xx

60.0 (Japanese varieties and genotypes). Differentiation in other seed traits fell within the so-far known cognizance.

Due to technical difficulties the collected forms were not assayed for protein and oil levels. Randomly, several dozen analyses were carried out. The protein level tended to be above 40% and the oil level above 16%. Also, initial screening was made for the presence of alleles of Kunitz trypsin inhibitor (SBTJ-A₂) and for alleles controlling the absence of the latter (Ti^o). This work has been continued with particular stress on establishing the genetic model of these phenomena, for use in breeding programs.

The data on 445 soybean forms, selected from field trials with 2412 varieties and lines in the years 1975-1977, revealed a wide variation range in phenological and morphological traits, as well as in seed yield parameters. They provide information about fairly large gene resources, sufficient to meet our present day breeding needs. Many lines are subjected to direct selection and tested for seed yield under strictly experimental conditions. The so-far available data for yielding capacity are regarded promising since the seed yield scores range from 1500 to 3000 kg/ha. Other forms which, along with distinct and economically valuable traits (e.g., high yielding capacity, good morphotype), carry less advantageous traits (late maturation), have been included into a complex crossing program.

The first stage of this program aims at suppressing the specific correlation between the early maturation and plant height. The very early forms are generally shorter and tend to set pods low, while medium and late maturing represent a very prospective morphotype. They are higher and have a relatively advantageous harvesting space. It seems that a recombination of the promising qualities and traits will be possible.

The three-year studies under varying weather conditions helped to a large extent to establish and/or set apart the genetic determination from the random variation. It appears that good grounds have been provided to expect a prospective recombinant variation from crossing.

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1) General ideas about soybean genetics.

I have seen pubescence, especially in nature plants, in brown color against gray color. The two types are equally frequent among commercial varieties. In brown pubescent genotypes the hairs in the young plants are colorless, but after a few weeks' growth, many of the hairs grow on the stems and pods and to a lesser extent on the leaves with brown pigments. In gray pubescent varieties only a few brownish hairs are formed and most hairs are without pigment, giving a distinct gray appearance to the fields of this kind of variety.

Black and brown pigments may occur in the outer layer of soybean seed coats in varying amounts and patterns.

In a few varieties the chlorophyll is retained in the ripe seed and also the leaves and pods; they don't turn yellow during ripening. This results in seeds that are green through, including cotyledons, embryo, axis and seed coat. This trait is often apparent at earlier season since leaf tissue killed by diseases or other factors doesn't turn yellow as in other varieties.

A coat, whitish or brownish bloom, occurs on some seed coats. Soybean, especially the young dark-seeded hay varieties, have a thin layer of apparently

the same material which gives the seeds a dull luster, whereas other varieties have little or none and exhibit a shiny seed coat. In soybean or any plant, the response of genotypes to space and to immediate neighbors constitutes a major component of reproductive ability. The differential response to space has been exploited successfully, at least with some genotypes, by utilization of narrow rows for commercial production. In the Middle East soybean production I have noticed the following: Up to 70% of the flowers produced by the plants may fall on the ground. The tendency of perfectly healthy flowers to abort is a major concern of the soybean workers. The technique for preventing this loss is not known yet. The plant loses more blossoms during periods of hot dry weather than in more favorable conditions. However, weather and fertility conditions that may be considered ideal still result in much flower drop. Therefore, the main reason for this drop is still unknown.

The Lee variety of soybean is highly popular in our area and is mainly preferred by our farmers.

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1) Underground pods in *Glycine falcata* Benth.

The genus *Glycine* L. has been divided into three sub-genera, namely *Glycine* L., *Bracteata* Verdc., and *Soja* (Moench) F. J. Herm. (Hymowitz, 1970). *G. falcata* of 1864 was the last of the true *Glycine* species to be described by Bentham (Hermann, 1962). *G. falcata* is one of the six species belonging to the sub-genus *Glycine* L. *G. falcata* appears to be restricted to Australia (Newell and Hymowitz, 1978).

From T. Hymowitz of the University of Illinois seeds of two *G. falcata* accessions (PI 233,139 and PI 246,519) were received. Scarified seeds were sown on 6 June 1979 in a 10 cm petri dish on a moistened filter paper. The seeds germinated on 9 June 1979. The seedlings were transplanted to 15 cm diameter pots containing a mixture of field soil : compost : sand : and rice straw in 1:1:1:1 ratio. The plants were exposed to 10 hr sunlight and then given 14 hr darkness every day. PI 246,519 flowered and produced mature pods in 114 and 155 days after sowing, respectively. PI 233,139 flowered in 77 days and

matured in 117 days.

The plants continued growth. Both the accessions produced roots at stem nodes in contact with the soil thereby giving rise to vegetatively reproduced daughter populations. In most of wild Glycine species such phenomena have been reported (Newell and Hymowitz, 1978). However, on G. falcata (PI 233,139) in addition to rooting at stem nodes, the nodes also bore almost sessile flowers in a cluster of 1 to 3. These flowers, since they are white in color, can be easily mistaken for root initials. The mature flower is about 4 to 5 mm in length. The calyx is appressed to the corolla and brown in color. The pedicels are very short, about 0.5 to 1.0 mm in length. Flowers are cleistogamous. The flowers remain inside the soil. Pods also developed inside the soil. The developing pods can be easily mistaken for Rhizobium root nodules. So far three pods have been harvested. All of them have developed from monocarpellary ovary. Pods are tan colored, 7 mm long with 4 mm maximum width. Each pod contained only one seed. Seed was yellow in color, 4 mm long and 2 mm wide. In contrast, the above-ground seed coat had black seed coat color with the same dimensions. PI 233,139 also produced normal flowers and three- to four-seeded pods above ground as described by Hermann (1962). Similar underground and above-ground pods have been reported in G. falcata (Everist, 1951; Hymowitz and Newell, 1975) and in the genus Amphicarpaea edgeworthii Benth. var. japonica Oliver which is called Yabumame in Japanese.

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2) Flowering of Glycine max (L.) Merr. with cotyledonary and unifoliolate leaves.

In 'Biloxi' soybeans the trifoliolate leaves are essential to perceive the photoperiodic inductive conditions and to cause the initiation of flower primordia (Borthwick and Parker, 1935). To respond to photoinduction, some plants have to reach "ripeness to flower" or pass the "juvenile phase" (Lang, 1965). "Juvenile phase" is distinct in some soybean cultivars, such as Acc. G 2120, while in the day-neutral soybean Acc. G 215 it is not clear whether there is a "juvenile phase" (Shanmugasundaram and Tsou, 1978). In both Acc. G 2120 and Acc. G 215 one trifoliolate leaf left on the short-day branch of a decapitated plant was able to induce flowering in both the short-day and leafless long-day branch (Shanmugasundaram et al., 1979). But when the long-day branch in Acc. G 2120 had four or more trifoliolate leaves the flower-inducing substance produced in the short-day branch could not induce flowers on the long-day branch (Shanmugasundaram et al., 1979). However, in Pharbitis nil (Kujirai and Imamura, 1958) and Chenopodium rubrum (Cumming, 1959) it has been demonstrated that the plants can be fully photoinduced at the cotyledonary leaf stage without any foliage to produce flowers. The experiment described in the present report demonstrates the flowering of a day-neutral soybean cultivar, Acc. G 215, with only the cotyledonary and the unifoliolate leaf left on the plant.

The photoperiod-sensitive soybean cultivar Acc. G 2120 and the day-neutral soybean cultivar Acc. G 215 were decapitated soon after the unifoliolate leaves emerged. Development of the two axillary buds from the unifoliolate leaf nodes was allowed. Axillary buds, if any developed at the cotyledonary leaf nodes, were removed. The plants were left in the 16-hour photoperiod. As the axillary buds developed, the trifoliolate leaves, before they unfolded, were continuously removed. The meristem was allowed to grow. From the time the branches were visible, one branch was exposed to a 10-hr photoperiod and the other branch in each plant was exposed to a 16-hr photoperiod. In one set of plants both branches were subjected to a 10-hr photoperiod. In another set of plants both branches were subjected to a 16-hr photoperiod. A set of decapitated plants with all the trifoliolate leaves present served as the control. The time from sowing to flowering of each branch and the total number of flowers produced were recorded.

Day-neutral Acc. G 215 plants with only cotyledonary and unifoliolate leaves flowered essentially in the same number of days as control plants with

all the trifoliolate leaves left on the plant (Table 1). Results suggest that the total number of flowers produced in the 10-hr photoperiod with cotyledonary and unifoliolate leaves were comparable to those with all the trifoliolate leaves present in the same photoperiod. The number of flowers are determined largely by the photoperiod (Table 1). In Acc. G 215 the cotyledons and the unifoliolate leaves not only perceive the photoperiodic stimulus but also provide sufficient photosynthate to saturate complete flowering quantitatively. The 16-hr photoperiod merely increased the photosynthate to produce more flowers.

Table 1
Flowering response of two branched day-neutral soybean, Acc. G 215
with and without trifoliolate leaves

Photoperiod on the decapitated plant's branches	No. of trifoliolate leaves on the two branches	Days to flowering of the two branches ⁺⁺	No. of flowers on the two branches ⁺⁺
10 h / 10 h	0 / 0 ⁺	50 / 49	14 / 18
16 h / 16 h	0 / 0 ⁺	50 / 48	21 / 21
10 h / 10 h	4 / 4	51 / 51	16 / 19
16 h / 16 h	8 / 8	51 / 48	20 / 29
10 h / 16 h	0 / 0 ⁺	49 / 50	13 / 20

⁺Cotyledonary and unifoliolate leaves alone remained on the plant.

⁺⁺Values are mean of 5 plants.

On the contrary, photoperiod sensitive Acc. G 2120 plants flowered only in the 10-hr branch with all the trifoliolate leaves present. The plants with only cotyledonary and unifoliolate leaves and the 16-hr branches with all the trifoliolate leaves did not flower. Therefore, it appears that flowering with only the cotyledonary and unifoliolate leaves may be under genetic control.

It is our belief that the above results constitute the first report of flowering in soybean with only cotyledonary and unifoliolate leaves in a day-neutral soybean plant. Efforts now are under way to study the role of cotyledonary leaf alone, unifoliolate leaf alone and trifoliolate leaf alone in the flowering of several day-neutral soybeans.

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1) Soybean mutation.

Since 1970, soybean radiation experiments have been conducted in Thailand. The objectives are (1) to create genetic variability in soybean cultivars by gamma radiation, and (2) to screen and to evaluate for desired characteristics with the aim of producing superior breeding lines with resistance to diseases and insects.

The purpose of this presentation is to report briefly the results obtained within a period of 1970 to 1977.

In general, the soybean seeds with moisture content between 10 and 14 percent were irradiated with gamma rays from a caesium source at the Division of Radiation and Isotopes, Kasetsart University. The M_2 seeds of each M_1 plant were usually sown as plant-to-row. The mutants were detected in the M_2 generation.

Two experiments were carried out in order to find a gamma radiation dose suitable for inducing mutation in 'Sansai' and 'S.J.2' cultivars. The doses were varied from 5 to 35 krad. It was found in one experiment that the maximum frequency of yellow seedlings in the M_2 generation occurred at 15 krad treatments. With this 15 krad dose, it was possible to obtain changes in morphological characteristics in later soybean experiments (Smutkupt, 1973; Smutkupt, 1976b). In an experiment using Sansai, 'S.J.1', S.J.2, 'Wakashima', and 'Cutler-71', yellow seedlings were observed in all cultivars with mutation

frequencies ranging from 0.09 to 0.53 percent. White-flowered mutants were obtained in the purple-flowered Wakashima with a frequency of 0.15 percent. White-flowered mutants were also observed in S.J.2. In brown-hilum cultivars, 0.09 percent black hilum mutants were observed in Wakashima and 0.14 percent in S.J.2, respectively (Singburaudom, 1977).

A lethal Sansai mutant with an extreme reduction in plant growth was obtained (Smutkupt, 1973).

In an experiment on cross pollination of white-flowered Sansai cultivar with two purple-flowered cultivars (S.J.1 and S.J.2), the natural outcrossing was not found in Sansai controls, but 0.04-0.18 percent of outcrossing were found in the Sansai plants grown from seeds treated with 15 krad (Jumnongnid, 1976; Jumnongnid and Smutkupt, 1977).

In respect to change in yield of mutant lines, it was not possible to obtain any single mutant line which yields statistical significantly higher than that of the control. The seed yield of mutants was always lower than that of the control (Channesri, 1975; Smutkupt, 1974; Smutkupt, 1975; Smutkupt, 1976a).

An increase in protein content was obtained in Sansai and S.J.2 mutants. The percentage of increment was approximately 2 to 3 percent (Smutkupt, 1975).

An increase, as well as a reduction, of about 1 percent oil content were observed in S.J.2 and Sansai mutants. In this experiment, the fatty acid composition of mutants and mutation-derived lines of both cultivars were determined. It was observed that there was 1 to 4 percent reduction of oleic acid in S.J.2 mutants, but a 2 to 6 percent increase in Sansai mutants. S.J.2 mutants had an increase of approximately 2 to 4 percent in linoleic acid and approximately 1 percent in linolenic acid. Conversely, Sansai mutants had approximately 2 to 4 percent reduction in linoleic acid and less than 1 percent reduction in linolenic acid (Channesri, 1975; Smutkupt, 1975).

The use of radiation as a tool for soybean improvement might be evident in an attempt to solve a problem of soybean rust, which is caused by Phakopsora pachyrhizi Syd. This is the most serious soybean disease in Thailand. A source of resistant genes for this disease is urgently needed. It is also very difficult to obtain the source in the germplasm collections.

In an experiment on the field evaluation on rust reaction in M_3 soybean lines, it was found that leaves on the upper third of the plants of three sub-lines derived from Line No. 123 (G 8375, and AVRDC accession), as well as one

out of three sublines derived from Line No. 138 (Taichung), were infected with non-sporulating lesions (332). The leaves in the upper third of the plants of other sublines including control lines were heavily covered with sporulating lesions (343) (Smutkupt *et al.*, 1978).

Soybean mutation experiments for inducing rust resistance are being carried out.

In conclusion, the data obtained from soybean radiation experiments show that gamma radiation can create variability in many characteristics of soybeans. However, when desired characteristics cannot be isolated from existing variability, then an attempt to create variability by radiation has considerable merit. Success in obtaining a desired characteristic, such as disease resistance, will depend largely on the effectiveness of screening techniques. The possibility of radiation-breeding as a useful tool for soybean improvement should not be overlooked.

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1) Observations of polyembryony and polyploidy in ms_1 and ms_2 male-sterile soybean populations.

Several reports of polyembryony and polyploidy in the progeny of ms_1 male-sterile soybeans have been made. Kenworthy *et al.* (1973) found 4% of 3485 seeds contained twin seedlings. Three triploids and one haploid were found among the twins. The seeds were from ms_1ms_1 plants of a locally adapted maintainer line. Palmer and Heer (1976) reported six sets of twins (2.9%) in 209 seeds examined. One twin plant was a triploid. Among 15 seedlings with abnormal cotyledons or roots, one was a tetraploid and eight had higher levels of ploidy; all other plants were diploid. The source of the seeds was ms_1ms_1 plants of 'Harosoy'. Beversdorf and Bingham (1977) obtained seeds from ms_1ms_1 plants of several genetic backgrounds and found 2.3% polyembryonic seeds in 7206. The frequency appeared somewhat lower in early maturing lines. A sample of 150 random monoembryonic seeds contained six (4%) triploids, but a sample of six small monoembryonic seeds contained five (83%) triploids. In addition, 61 monoembryonic seedlings that were from shriveled seeds or had germinated slowly produced nine triploids, two tetraploids, three pentaploids and two hexaploids.

The objective of our study was to obtain tetraploid plants for further study. Separate populations containing the ms_1 and ms_2 genes were surveyed. M1-MS78 contained bulked seeds from ms_1ms_1 plants from a composite population that was three generations removed from crosses of several adapted lines and varieties with N69-2774, the source of ms_1 . M2-MS78 contained bulked seeds from ms_2ms_2 plants of a similar population derived from crosses of

adapted lines and varieties with L74-01, the source of \underline{ms}_2 . Both populations had been maintained in isolation from each other but no attempt was made to restrict pollination from other nearby soybeans. The male-sterile plants in each population were typical of the descriptions of their respective male-sterile sources.

A random sample of seeds from each population was germinated in sand in the greenhouse. In addition a small sample of shriveled seeds and large seeds was selected from each population and germinated. Chromosome counts were attempted on all the above seedlings as well as a few late germinating seedlings taken from another sample of the same populations.

Approximately seven days after planting the seedlings were lifted, a few root tips removed and the seedlings replanted. Root tips were pretreated in a saturated paradichlorobenzene solution for an hour and a half and fixed in a solution of 3 parts ethanol to 1 part glacial acetic acid. They were hydrolyzed in 1N HCl for six min at 55°C and then squashed in aceto-carmin stain.

As shown in Table 1 no polyembryonic seeds were found in the \underline{ms}_1 population. Based on frequencies cited in other reports, our sample should have contained four to seven sets of multiple seedlings. Table 2 shows that only one triploid was present in 139 seedlings examined in M1-MS78. All other plants were diploid. These are clearly lower frequencies than found in previous reports. One similarity is that the single observed triploid did arise from a shriveled seed. Beversdorf and Bingham (1977) also found a much higher frequency of polyploids from small and shriveled seeds.

Based on the observations in this study and others, it appears that either genetic background or environment or both can influence the frequency of polyembryonic and polyploid progeny of $\underline{ms}_1\underline{ms}_1$ plants. Kenworthy *et al.* (1973) found that the frequency of polyembryonic seeds ranged from 2.2% to 5.5% over a period of three successive years. Also, Beversdorf and Bingham (1977) observed some variation among different genetic backgrounds.

As shown in Table 1, the \underline{ms}_2 population exhibited a higher frequency of polyembryonic seeds than was observed in the \underline{ms}_1 population. In fact, the frequency observed approaches that reported in the previously cited studies of the progenies of $\underline{ms}_1\underline{ms}_1$ plants. Also, the frequency of polyploids observed in M2-MS78 is similar to that observed in M1-MS78 (Table 2). Although the number of observations perhaps is not large enough to draw conclusions, these comparisons indicate that the level of polyembryony and polyploidy in the \underline{ms}_2 population is at least as high as that observed in the \underline{ms}_1 population.

Table 1
Observations of polyembryony in two male-sterile populations

Sample	M1-MS78		M2-MS78	
	No. seeds germ.	No. twins	No. seeds germ.	No. twins
Random seeds	168	0	137	1
Shriveled seeds	5	0	11	0
Large seeds	3	0	5	1

Table 2
Observations of polyploidy in two male-sterile populations

Sample	M1-MS78		M2-MS78	
	No. seedlings examined	No. polyploids	No. seedlings examined	No. polyploids
Random seeds	123	0	88	1 ⁺
Shriveled seeds	5	1 ⁺	11	0
Large seeds	3	0	5	0
Late germ. seedlings	8	0	2	0

⁺Both polyploid seedlings were triploids.

This implies that the ms₂ gene causes meiotic irregularities similar to those caused by the ms₁ gene. The fact that ms₂ms₂ plants are usually more fertile than ms₁ms₁ plants indicates that there might be some differences in the mechanisms causing polyembryony and polyploidy in each. A cytological comparison would be necessary to determine the validity of this assumption.

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1) Rhizobium japonicum inoculation on Glycine max in Vietnam.

Reference has been made to the culture of soybeans (Glycine max [L.] Merrill) in Vietnam by Louriro (1793) and Rumphius (1747) as far back as the eighteenth century. Wild soybean (Glycine laotica) is present in Vietnam, having been collected by Harmand (1877) in the area of Hue and the Bassac River in the 19th century. Kwon (1969) speculated that since the history of Vietnam is related closely with China, there is little doubt that soybeans have been grown for many centuries in this country. However, observation and discussion by the authors have failed to reveal any significant nodulation on soybeans grown in the specific area under consideration, that is, in the N.W. area of the Vietnamese Mekong Delta approximately delimited by 105° to 106° E longitude and 9°50' to 10°50' N latitude.

Producers in the area who grow soybeans presently fertilize with urea in amounts up to 500 kg/hectare. Smith (1971) in discussing soybean production in the Philippines, states that few persons understood or had knowledge of the role played by nodulating bacteria on the roots of plants. This observation also would be applied to Vietnam. Smith further comments that the use of nitrogen fertilizer on soybeans in the Philippines should be omitted, that the advantage of growing a legume is lost if the expense of applying nitrogen is added to production costs. In countries where soybeans are grown commercially on a large scale, the benefit of inoculation with R. japonicum is known and its practice recommended. Jackson (1971) states that research to date in the United States has revealed few benefits from applying supplemental nitrogen to well-nodulated soybeans.

Jackson recommends that soybean seed be treated with molybdenum at the same time as inoculation. Molybdenum is a trace element essential in the nitrogen-fixing process. Jackson reports that, in Georgia research trials, yields have been doubled by the use of only one ounce of molybdenum salt per acre. Georgia research has suggested that much of soybeans response to lime may be largely a response to molybdenum. This trace element is less available in acid soils. Liming to neutralize soil acidity makes molybdenum more available to the soybean plant.

Materials and methods: The soybean variety 'Palmetto' (a locally common variety) was planted in a randomized complete block design with four replications. Plot size was 6 m x 5 m, with 5 m rows spaced at 50 cm and an intrarow seed spacing of 5 cm. Planting was made on January 13, and plots harvested on April 15. Seed was hand-planted to a depth of 1.5 cm and all seed treatments were carried out immediately prior to planting. All plots were band fertilized 5 cm below and to the side of the seed at a rate of 0-60-60. TSP was the source for P205, and KCl the source for K20.

Treatments were as follows:

- a) control
- b) molybdenum seed treatment
- c) molybdenum seed treatment + Rhizobium inoculation
- d) Rhizobium inoculation
- e) 23-0-0 (urea source)
- f) molybdenum seed treatment + 23-0-0
- g) molybdenum seed treatment + Rhizobium treatment + 23-0-0
- h) Rhizobium inoculation + 23-0-0

Where applicable, a solution of 1 gm of Na_2MoO_4 per kilo seed was used to wet the seed immediately before planting. Also where applicable, seed was inoculated with a commercial preparation (humus base) of 'Nitragin' for soybeans, supplied by the Nitragin Company, Milwaukee, Wisconsin. Sweetened condensed milk was used as an adhesive for the inoculum on the moistened seed. Seed was planted immediately after inoculation.

The experiment was planted on recent to semi-recent alluvium with a surface reaction of $\text{pH } 5.0 \pm 0.2$, and a very heavy clayey texture. This brown alluvium is high in calcium and magnesium, while very low in phosphorus and predicted nitrogen. The area is subjected to annual continuous flooding during September, October and November. Soybeans are not extensively grown in

the area, nor is there evidence of established Rhizobium specific for soybeans. Therefore, inoculation was able to be included as a valid variable in the experiment.

Discussion: The intent of the experiment was to determine whether the present use of nitrogen fertilization on non-nodulated soybeans as practiced by the producers in Vietnam could be substituted by proper inoculation of the seed. Molybdenum was entered as a variable to determine its value on rhizobial activity in the acidic soil regime.

The results (Table 1) indicate with a high level of statistical significance that Rhizobium inoculation when combined with a seed treatment of molybdenum can produce yields of soybean higher than those from an application of N at 23 kg/ha. It would appear that, in these acid soils, the added molybdenum is essential for proper functioning of the Rhizobium, since inoculation alone did not give significantly higher yields over the control, yet produced adequate numbers of nodules.

Table 1

Treatment	Replication ^a				Mean
	I	II	III	IV	
a	1.01	2.22	0.62	0.95	1.20
b	1.49	1.56	1.66	0.67	1.35
c	1.81	2.50	2.00	1.09	1.85
d	2.90	4.72	2.77	3.05	3.36**
e	1.46	4.03	2.83	1.19	2.38*
f	1.86	3.51	1.68	1.30	2.09
g	3.05	3.40	4.07	3.01	3.38**
h	1.29	4.71	1.27	2.44	2.43*

^aYield in kg/plot.

Table 2
Analysis of variance

Source of variation	d.f.	SS	Mean SS	F
Replications	3	13.04		
Treatments	7	18.68	2.67	20.91
Error	21	9.20	0.44	

LSD_(.01) : 1.33 kg/plot

LSD_(.05) : 0.98 kg/plot

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1) Inheritance of pubescence color and reactions to three viruses in the cross York x Lee 68.

Three viruses are prevalent on soybean in the peanut producing counties of Virginia. These are peanut mottle virus (PMV), peanut stunt virus (PSV) and soybean mosaic virus (SMV). Each may cause extensive yield losses among

susceptible soybean cultivars under certain conditions. Generally, 'York' has remained virus-free in most of Virginia and we have found that it is resistant to PMV and SMV but susceptible to PSV. York is a selection of the cross 'Dorman' x 'Hood' and apparently derived its resistance to SMV from Hood and its resistance to PMV from Dorman. The latter is probably conditioned by the gene Rpv₁ (Shipe et al., 1979). York has gray pubescence (tt) (Bernard and Weiss, 1973). The cultivar 'Lee 68' is susceptible to PMV and SMV but resistant to PSV; it has tawny pubescence (TT). The origin of resistance to PSV is unknown.

In order to study the inheritance of reaction to the three viruses, PMV, PSV and SMV, we made the cross York x Lee 68. Since reaction to only one virus may be determined for an individual F_2 plant, we grew and harvested the F_3 seed from 623 F_2 plants. The seeds of each F_3 line were partitioned into 3 equal portions and 623 rows in each of 3 separate blocks were planted in field plots. When the plants reached the unifoliolate-to-first-trifoliolate-leaf stage, they were inoculated with PMV, PSV or SMV. Infected plants were counted and removed 3 weeks after they were inoculated and the remaining plants were reinoculated with the same virus as before. Again, virus-infected plants were removed and counted. In addition, the number of healthy plants was recorded. From these counts, rows had only virus-free plants (= resistant, R), had infected and virus-free plants (= heterozygous, H), or had all plants infected (= susceptible, S). The phenotype for pubescence color was also recorded. From these data, the genotype for reaction to each virus and for pubescence color of each F_2 plant was determined. Since resistance is completely dominant for each virus and tawny pubescence is also completely dominant, the phenotype of each F_2 plant is also known. The progenies of 10 F_1 plants were studied and designated as families. Homogeneity for 10 families was also determined. Our observations may be summarized, as shown in the table on the next page.

From a careful examination of the data, including total Chi-squares and Chi-squares for pooled data, Tt, PMV, and SMV were found to be conditioned by monogenic dominant genes. Reaction to PSV is probably monogenic dominant but due to problems with inoculation efficiency, further study is required before a hypothesis can be validated. For this reason, the 9:3:3:1 ratio was not obtained with pairs of characters when one character was reaction to PSV.

Table 1

Number of families fitting ratio and homogeneity of families

Character or gene	Phenotypic ratio, 3:1	Homogeneous 3:1	Genotypic ratio, 1:2:1	Homogeneous 1:2:1
<u>Tt</u>	10	yes	9	yes
PMV reaction	10	yes	8	yes
SMV reaction	10	yes	9	yes
PSV reaction	6	yes	6	no

Pairs characters	Number of families fitting 9:3:3:1	Homogeneous
<u>Tt</u> , PMV	10	yes
<u>Tt</u> , SMV	10	yes
<u>Tt</u> , PSV	8	yes
PMV, SMV	0	yes
PMV, PSV	8	yes
SMV, PSV	8	yes

No fit to the 9:3:3:1 ratio was obtained for the SMV, PMV pair because there was a very low number of recombinants. By Immer's (1930) product method, we calculated the linkage intensity for SMV, PMV at 3.7%. We observed that reactions to SMV and PMV were segregating independently of Tt.

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1) Frequency of spectrum of visible mutations induced by gamma rays in soybean.

Although mutation studies are very common in most of the crop plants, soybean (Glycine max [L.] Merrill.) has received comparatively little attention by the mutation breeders. In view of this, systematic mutation studies were started at Ranchi Agriculture College, Kanke. The present study reports the effect of gamma rays on the frequency and spectrum of visible mutations in soybean.

Materials and methods: Seeds of a soybean variety Sepaya Black, brought to uniform moisture content, were irradiated with gamma rays at Fertilizer Corporation of India, Sindri, Dhanbad (Bihar) at a dose of 10 kr, 20 kr, 30 kr, and 40 kr. One hundred seeds of each radiation treatment and control were sown in single rows having 45 cm distance between the rows and 30 cm between the plants at the experimental area of Ranchi Agricultural College, Kanke, Ranchi during the rainy season of 1971.

Twenty seeds of each R_1 plants selected at random were sown separately in individual plant-to-progeny rows in the rainy season of 1972. All the seed of those R_1 plants were sown which were containing less than twenty seeds.

Scoring for visible mutants was done when plants started germination and continued during the entire life cycle prior to harvest. Mutation frequency was calculated as (1) the percentage of R_1 plant progenies segregating, (2) as percentage of mutants per R_2 family, and (3) as percentage of mutants in R_2 population. Twenty-four soybean genetic type collection mutants obtained from Dr. R. L. Bernard, Research Geneticist, U.S. Regional Soybean Laboratory, Urbana, Illinois, were also used for comparison of the visible mutants obtained in the R_2 generation.

Results and discussion: Frequency and rate of visible mutations in R_2 -- The frequency and rate of visible mutations observed in the R_2 generation were calculated. The data indicate that the frequency of visible mutants based on segregating families was 10.98, 7.69 and 9.67 percent in 10, 20 and 30 kr respectively. There was no expression in R_2 plants for visible mutations in 40 kr dose. This may be due to very small population available for study in

40 kr dose. The frequency of visible mutations calculated on the basis of per 100 R_2 families was 10.98% in 10 kr, 7.69% in 20 kr and 16.12% in 30 kr. The frequency of mutants calculated on the basis of per 100 R_2 plants was 0.76, 0.81 and 1.60% in 10, 20 and 30 kr. The total frequency of mutants observed in R_2 was 9.17, 10.83 and 0.95% based on segregating families, mutants per 100 R_2 families and mutants per 100 R_2 plants. The results, thus, indicate that the total frequency of visible mutations do not follow any particular trend. Gaul (1964), however, reported a dose dependent increase in segregating ratios with increase in doses with other crop plants. The three methods used for calculating the frequency of visible mutations gave different results. The frequency of visible mutations was maximum in 10 kr, when calculated on the basis of R_1 segregating families, while it was maximum in 30 kr, when calculated on the basis of per 100 R_2 families and 100 R_2 plants. Humphery (1951) reported the results of an experiment in which the seeds of the soybean variety Dortchsoy 2 was subjected to neutron irradiations. In the R_2 generation, 228 mutant plants were observed out of a population of 4,200 plants. Humphery (1951), however, did not make any attempt to classify the mutants obtained in his study into those affecting quantitative traits (micro-mutations) and those affecting qualitative traits (macro-mutations).

Spectrum of visible mutation and relative frequency of different types-- The different types of mutants with their relative frequency and spectrum were estimated. The mutations observed in R_2 have been classified under three broad classes: (1) chlorophyll deficient types, (2) leaflet types, and (3) rugose plant type.

Chlorophyll deficient types--lethal mutant: One lethal mutant was observed in 20 kr dose which died at cotyledon stage after 14 days of sowing. This mutant was completely bright yellow and expressed this characteristic at the very beginning of its emergence after germination. The spectrum of this type of mutant was 14.29% out of the total chlorophyll deficient types. Weber and Weiss (1959) have also reported lethal yellow plant in soybean for which the gene symbol y_{11} has been assigned by them.

Light yellow-green leaves: The leaves of this chlorophyll deficient type became light yellow from complete green color. The plants having light yellow green leaves were weak and had less number of pods. One plant of this type was observed in 20 kr, while there were five plants in 30 kr. The spectrum of this chlorophyll deficient type was 85.71% out of the total chlorophyll

deficient types.

In the present study, no chlorophyll deficient type was isolated in 10 kr, while one plant in 20 kr and 5 plants in 30 kr were obtained. The results, thus, indicate that the frequency of this chlorophyll deficient type was dose dependent. This finding is in agreement with similar reports in other crop plants (Gaul, 1964).

Leaflet types: Normally soybean plant has three leaflets. In the present study, two, four, five and six leaflet types were obtained over the normal three leaflet. Only one plant having 'two-leaflet' type was observed in 10 kr while 7, 2 and 2 plants having the 'four leaflet' were observed in 10, 20 and 30 kr doses respectively. The number of 'five leaflet' type plants observed was 2, 2 and 1 respectively in 10, 20 and 30 kr. One plant having 'six leaflet' type was also observed in 30 kr. Out of the total different leaflet types isolated, the spectrum of two-leaflet, four-leaflet, five-leaflet and six-leaflet types were 5.55, 61.11, 27.78 and 5.55% respectively. The results, thus, indicate that the frequency of 'four-leaflet' type was maximum among the different leaflet types isolated in the present study. The frequency of leaflet types, however, did not follow any particular trend.

Rugose plant type: In the present study, one plant was observed in 30 kr characterized by dark green and wrinkled leaves. This mutant was identified as 'Rugose' plant. The percentage of this mutant type was 3.85 out of total macro-mutants isolated in the present study. Plants possessing such a characteristic have also been isolated by Humphery (1951) following neutron irradiation in the Dortchsoy 2 variety of soybean and has been named as 'Rugose' plant type.

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